



Qy	61	CAAAAGAGCTGCCAGACGACGCGCCCTCTGGCGTCCGCCGCCCCCAACACGAGCGAGCGGA	120
Db	61	CAAAAGAGCTGCCAGACGACGCGCCCTCTGGCGTCCGCCGCCCCCAACACGAGCGAGCGGA	120
Qy	121	GCGAACGCGACAGGGGGGAGAGTGCACACTCTCAAGCAAGGGGGTTTGTAAAGCAGTGA	180
Db	121	GCGAACGCGACAGGGGGGAGAGTGCACACTCTCAAGCAAGGGGGTTTGTAAAGCAGTGA	180
Qy	181	TGTCATAATGATGTAATGCTTATGTCACGGGATAGTTAATTAAGTAACAGTCAATGTGATG	240
Db	181	TGTCATAATGATGTAATGCTTATGTCACGGGATAGTTAATTAAGTAACAGTCAATGTGATG	240
Qy	241	TGTTTTATCCAAATAGAGAAAGCGCGGTATGAGTTCTCGGAGACTTCGCGGGGTATAA	300
Db	241	TGTTTTATCCAAATAGAGAAAGCGCGGTATGAGTTCTCGGAGACTTCGCGGGGTATAA	300
Qy	301	AAGACCGAGTGAAACGAGCGCGCGCATCTTTGCTCTGGACTGTAGAGACCCCTCGCT	360
Db	301	AAGACCGAGTGAAACGAGCGCGCGCATCTTTGCTCTGGACTGTAGAGACCCCTCGCT	360
Qy	361	GCCATGGCTACCTTCTATGAAAGTCAATGTTTCGGTCCCATTTTGAAGTGAAGAAACATCTG	420
Db	361	GCCATGGCTACCTTCTATGAAAGTCAATGTTTCGGTCCCATTTTGAAGTGAAGAAACATCTG	420
Qy	421	CCTGGAATTTCTGACAGCTTTCTGGACTGGTAACTGGTCAAAATTTGGGAGCTGCTCCA	480
Db	421	CCTGGAATTTCTGACAGCTTTCTGGACTGGTAACTGGTCAAAATTTGGGAGCTGCTCCA	480
Qy	481	GAGTCAGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACCGTGGCTGATGAATTT	540
Db	481	GAGTCAGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACCGTGGCTGATGAATTT	540
Qy	541	CGCGCGTGTCTCTGTAAGTGGAAACAAATTTTCAAGCAGAGTCCAAATTTCTTTGTG	600
Db	541	CGCGCGTGTCTCTGTAAGTGGAAACAAATTTTCAAGCAGAGTCCAAATTTCTTTGTG	600
Qy	601	CAGTTTGAAGAGGATCTGATATTTTCACTGACACAGCTGTGAGAGCCTCCGCGATC	660
Db	601	CAGTTTGAAGAGGATCTGATATTTTCACTGACACAGCTGTGAGAGCCTCCGCGATC	660
Qy	661	TCTTCCATGCTCTCGCGCGCTACGTGAGTCAAGTTCGCGCCAGCTGGTGAAGTGGTC	720
Db	661	TCTTCCATGCTCTCGCGCGCTACGTGAGTCAAGTTCGCGCCAGCTGGTGAAGTGGTC	720
Qy	721	TTCCAGGGATTTGAACCCCGAGATCAACGACTGGGTGCGCATCACCAGGTAAAGAGGGC	780
Db	721	TTCCAGGGATTTGAACCCCGAGATCAACGACTGGGTGCGCATCACCAGGTAAAGAGGGC	780
Qy	781	GGAGCCAATAAGTGTGATTTCTGGGTATATTCGCGCCTACCTGCTGCCGAAGTCCAA	840
Db	781	GGAGCCAATAAGTGTGATTTCTGGGTATATTCGCGCCTACCTGCTGCCGAAGTCCAA	840
Qy	841	CCGAGCTTCAGTGGCGTGGACAAACCTGGACGAGTATAAATTTGGCGCGCTGATCTG	900
Db	841	CCGAGCTTCAGTGGCGTGGACAAACCTGGACGAGTATAAATTTGGCGCGCTGATCTG	900
Qy	901	GAGGAGGCHAAACGGCTCGTGGCAGTTTCTGGCAGAAATCCTCGCAGCGCTCGCAGGAG	960
Db	901	GAGGAGGCHAAACGGCTCGTGGCAGTTTCTGGCAGAAATCCTCGCAGCGCTCGCAGGAG	960
Qy	961	GCGGCTTCGAGGCTGAGTTCTGGCTGACCCCGTCAATCAAAAGCAAGACTTCCCGAGAA	1020
Db	961	GCGGCTTCGAGGCTGAGTTCTGGCTGACCCCGTCAATCAAAAGCAAGACTTCCCGAGAA	1020
Qy	1021	TACATGCGCTCGTCAACTGGCTGGAGACGCGATCACTTCCGAGAGCAGTGGATC	1080
Db	1021	TACATGCGCTCGTCAACTGGCTGGAGACGCGATCACTTCCGAGAGCAGTGGATC	1080
Qy	1081	CAGGAAATCAGGAGGACTACTCTCTCACTCCACCGGCACTCTCGAGCGAGTC	1140
Db	1081	CAGGAAATCAGGAGGACTACTCTCTCTCTCACTCCACCGGCACTCTCGAGCGAGTC	1140

Qy	1141	AAGCCGCGCTCGACAAACGCGACCAAAATTAATAGTCTGACAAAAAGCGCGTGGACTAC	1200
Db	1141	AAGCCGCGCTCGACAAACGCGACCAAAATTAATAGTCTGACAAAAAGCGCGTGGACTAC	1200
Qy	1201	CTCGTGGGAGCTCGGTTCGCGAGACATTTCAAAACACAAATCTGCAAAATTTTTCAG	1260
Db	1201	CTCGTGGGAGCTCGGTTCGCGAGACATTTCAAAACACAAATCTGCAAAATTTTTCAG	1260
Qy	1261	ATGAATGCTACGACCCGCGCTACGCGGATCCATCTCTACGGTGGTGTGTCAGCGCTCC	1320
Db	1261	ATGAATGCTACGACCCGCGCTACGCGGATCCATCTCTACGGTGGTGTGTCAGCGCTCC	1320
Qy	1321	TTCAACAGAGGAAACACCGTCTGCGACCCGCGCACACCGCGGCAAGCAACATC	1380
Db	1321	TTCAACAGAGGAAACACCGTCTGCGACCCGCGCACACCGCGGCAAGCAACATC	1380
Qy	1381	GCGAGGCGCATCGCCACACTGTGCGCTTTTACGGCTGGTGAATGACCCNATGAAAC	1440
Db	1381	GCGAGGCGCATCGCCACACTGTGCGCTTTTACGGCTGGTGAATGACCCNATGAAAC	1440
Qy	1441	TTTCCCTTTAATGACTGTGTGGACAAATGCTCATTTTGGTGGAGGAGGAAAGATGACC	1500
Db	1441	TTTCCCTTTAATGACTGTGTGGACAAATGCTCATTTTGGTGGAGGAGGAAAGATGACC	1500
Qy	1501	AACAAAGTGGTTGAATCCGCCAAGCCCATCTGGGGGGCTCAAAAGTGGCGGTTCGATCAG	1560
Db	1501	AACAAAGTGGTTGAATCCGCCAAGCCCATCTGGGGGGCTCAAAAGTGGCGGTTCGATCAG	1560
Qy	1561	AAATGTAATCCTCTGTTCAAAATTCATTTACCCCTGTCAATTTGAATTTTCCAATCAAAAC	1620
Db	1561	AAATGTAATCCTCTGTTCAAAATTCATTTACCCCTGTCAATTTGAATTTTCCAATCAAAAC	1620
Qy	1621	ATGTGTGTGGTGGATGGGAAATTCACGACCTTTTGAAACACGACGCGCGTGGAGGAC	1680
Db	1621	ATGTGTGTGGTGGATGGGAAATTCACGACCTTTTGAAACACGACGCGCGTGGAGGAC	1680
Qy	1681	CCCATGTTCAAAATTTGAACGCTGATGAGCGGCTCCGCCAGATTTTGGCAAGATTACTAAG	1740
Db	1681	CCCATGTTCAAAATTTGAACGCTGATGAGCGGCTCCGCCAGATTTTGGCAAGATTACTAAG	1740
Qy	1741	CAGGAAGTCAAGGACTTTTTCCTGGGCAAAAGTCAATCAGGTGCGGTGACTCACGAG	1800
Db	1741	CAGGAAGTCAAGGACTTTTTCCTGGGCAAAAGTCAATCAGGTGCGGTGACTCACGAG	1800
Qy	1801	TTTAAAGTTCCAGGGAATTTGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCCA	1860
Db	1801	TTTAAAGTTCCAGGGAATTTGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCCA	1860
Qy	1861	CTGGGTGAGCTCACCAATAGTATTAAGTCTGGAGAGCGGCGGAGGCTCTCATTT	1920
Db	1861	CTGGGTGAGCTCACCAATAGTATTAAGTCTGGAGAGCGGCGGAGGCTCTCATTT	1920
Qy	1921	GTTCGCGAGCGCTCGCAGTTTCAGAGTTCAGAGTTCAGTGTGATCCCGCTCTCTGCGACGCTC	1980
Db	1921	GTTCGCGAGCGCTCGCAGTTTCAGAGTTCAGAGTTCAGTGTGATCCCGCTCTCTGCGACGCTC	1980
Qy	1981	AATTTGAATTTCAAGGTATGATTTGCAAAATGATATCATGTCTCAATTTGACAAATTTCT	2040
Db	1981	AATTTGAATTTCAAGGTATGATTTGCAAAATGATATCATGTCTCAATTTGACAAATTTCT	2040
Qy	2041	AACAAATGATGAATTTGAATTCGCGGCAAAATGATGATGATGATGATGATGATGATGAT	2100
Db	2041	AACAAATGATGAATTTGAATTCGCGGCAAAATGATGATGATGATGATGATGATGATGAT	2100
Qy	2101	GTAACCTCACTGTCAAAATTTGTCTATGGGATTTCCCGCTGGGAAAGGAAACTTGTTCAGAT	2160
Db	2101	GTAACCTCACTGTCAAAATTTGTCTATGGGATTTCCCGCTGGGAAAGGAAACTTGTTCAGAT	2160
Qy	2161	TTTGGGATTTTGAAGTGCATTAAGAAACAGTAAATAAGCGAGTAGTCACTGCTCTTT	2220
Db	2161	TTTGGGATTTTGAAGTGCATTAAGAAACAGTAAATAAGCGAGTAGTCACTGCTCTTT	2220
Qy	2221	GTTCATCACCCCTCCAGATTTGGTGGAGAAAGTTGGTGAAGGTCTTCGCGAGTTTTCGGC	2280

Db 2221 GTTGATCCCTCCAGATTGGTTGAAGAAGTTGGTGAAGTCTTCGCGAGTTTGTGGC 2280  
QY 2281 CTTGAAGGGGGCCACCAGAACCAAAACCAATCAGCAGCATCAGATCAAGCCCGTGGT 2340  
Db 2281 CTTGAAGGGGGCCACCAGAACCAAAACCAATCAGCAGCATCAGATCAAGCCCGTGGT 2340  
QY 2341 CTTGTGCTGCTGGTTAATACTATCTCGGACCCGGAAACGGTCTCGATCGAGGAGGCT 2400  
Db 2341 CTTGTGCTGCTGGTTAATACTATCTCGGACCCGGAAACGGTCTCGATCGAGGAGGCT 2400  
QY 2401 GTCACAGGGCAGAGGTCGCGGAGAGCAGCAGATCTCGTACAAAGCAGCTTGAG 2460  
Db 2401 GTCACAGGGCAGAGGTCGCGGAGAGCAGCAGATCTCGTACAAAGCAGCTTGAG 2460  
QY 2461 GCGGGAGACAAACCTTCTCAAGTACAAACCAACCGGAGCGGAGTTCAGGAGAGCTC 2520  
Db 2461 GCGGGAGACAAACCTTCTCAAGTACAAACCAACCGGAGCGGAGTTCAGGAGAGCTC 2520  
QY 2521 GCCGACGACATCCTTTGGGGGAAACCTCGGAAAGGAGTCTTTTCAAGGCCAAGAAAGG 2580  
Db 2521 GCCGACGACATCCTTTGGGGGAAACCTCGGAAAGGAGTCTTTTCAAGGCCAAGAAAGG 2580  
QY 2581 GTTCTCGAACCTTTTGGGCTGGTTGAAGAGGTCGTAAGACGGGCCCTTACCGGAAAGCGG 2640  
Db 2581 GTTCTCGAACCTTTTGGGCTGGTTGAAGAGGTCGTAAGACGGGCCCTTACCGGAAAGCGG 2640  
QY 2641 ATAGACGACCACTTTCCAAAGAAAGAGGCTCGGACCGGAGTCCAGGATCCAGGCCAA 2760  
Db 2641 ATAGACGACCACTTTCCAAAGAAAGAGGCTCGGACCGGAGTCCAGGATCCAGGCCAA 2760  
QY 2701 ACTCTGTACAGCGCGAGTGGACCCAGCGGATCCAGGAGTCCAGGATCCAGGCCAA 2760  
Db 2701 ACTCTGTACAGCGCGAGTGGACCCAGCGGATCCAGGAGTCCAGGATCCAGGCCAA 2760  
QY 2761 CCAGCTCAAGTTTGGAGCTGATACAAATGCTCTCGGGAGGTCGCGGCCATTTGGGGGAC 2820  
Db 2761 CCAGCTCAAGTTTGGAGCTGATACAAATGCTCTCGGGAGGTCGCGGCCATTTGGGGGAC 2820  
QY 2821 AATAACCAAGTGCAGTGGAGTGGCAATGCTCTCGGGAGGTCGCGGCCATTTGGGGGAC 2880  
Db 2821 AATAACCAAGTGCAGTGGAGTGGCAATGCTCTCGGGAGGTCGCGGCCATTTGGGGGAC 2880  
QY 2881 TGGATGGGGACAGAGTCGTCAACAGTCCACCGGACCTGGGTGCTGCCAGCTACAAC 2940  
Db 2881 TGGATGGGGACAGAGTCGTCAACAGTCCACCGGACCTGGGTGCTGCCAGCTACAAC 2940  
QY 2941 AACCCAGTACGAGAGATCAAAAGCGGCTCGGTGACGGAAGCAACGCCACGCTAC 3000  
Db 2941 AACCCAGTACGAGAGATCAAAAGCGGCTCGGTGACGGAAGCAACGCCACGCTAC 3000  
QY 3001 TTTTGGATACAGCACCCCTGGGGGTACTTTGACTTTTAAACGCTTCCACAGCCACTGGAGC 3060  
Db 3001 TTTTGGATACAGCACCCCTGGGGGTACTTTGACTTTTAAACGCTTCCACAGCCACTGGAGC 3060  
QY 3061 CCCCGAGATGGCAAGACTCATCAACACTACTGGGGCTTCAGACCCCGGTCCTCAGA 3120  
Db 3061 CCCCGAGATGGCAAGACTCATCAACACTACTGGGGCTTCAGACCCCGGTCCTCAGA 3120  
QY 3121 GTCAAAATCTTCAACATTCAGTCAAGAGGTCAAGGTGAGGACTTCCACCAACCATC 3180  
Db 3121 GTCAAAATCTTCAACATTCAGTCAAGAGGTCAAGGTGAGGACTTCCACCAACCATC 3180  
QY 3181 GCCAACAACTCCTCCACCGTCCAAGTGTTTTACGAGCAAGCACTACAGCTGCCCTAC 3240  
Db 3181 GCCAACAACTCCTCCACCGTCCAAGTGTTTTACGAGCAAGCACTACAGCTGCCCTAC 3240  
QY 3241 GTCGTGGCAACCGGACCGAGGATGCTGCCGGCTTCCCTCCGAGGTCCTTTAAGCTG 3300  
Db 3241 GTCGTGGCAACCGGACCGAGGATGCTGCCGGCTTCCCTCCGAGGTCCTTTAAGCTG 3300  
QY 3301 CCGCAGTACGGTACCGGAGCTGAACCGGCAACACAGAAATCCGACCGAGAGGAGC 3360

Db 3301 CCGCAGTACGGTTAGCGACGCTGNAACCGCAGCAACACAGAAATCCCAACCGAGGAGC 3360  
QY 3361 AGCTTCTTCTGCTTAGAGTACTTTCCCAAGCAAGATGCTGAGAACGGGCAACACTTTTGAG 3420  
Db 3361 AGCTTCTTCTGCTTAGAGTACTTTCCCAAGCAAGATGCTGAGAACGGGCAACACTTTTGAG 3420  
QY 3421 TTTTACCTACAACTTTGAGGAGTGGCTTCCACTCCAGTTCGCTCCAGTCAAGACCTG 3480  
Db 3421 TTTTACCTACAACTTTGAGGAGTGGCTTCCACTCCAGTTCGCTCCAGTCAAGACCTG 3480  
QY 3481 TTCAAGCTGGCAACCCCGCTGGTGGACCACTTGTACCGCTTCTGTCAGCAACAATAC 3540  
Db 3481 TTCAAGCTGGCAACCCCGCTGGTGGACCACTTGTACCGCTTCTGTCAGCAACAATAC 3540  
QY 3541 ACTGGCGAGTTCAGTTCACAAAGAACTGGCCGGGAGATACGCCAACACTTACAAAAC 3600  
Db 3541 ACTGGCGAGTTCAGTTCACAAAGAACTGGCCGGGAGATACGCCAACACTTACAAAAC 3600  
QY 3601 TGGTTCCCGGGGCCCATGGGCCGGAACCCAGGCTGGAACTGGGCTCGGGGTCAACCGC 3660  
Db 3601 TGGTTCCCGGGGCCCATGGGCCGGAACCCAGGCTGGAACTGGGCTCGGGGTCAACCGC 3660  
QY 3661 GCCAGTGTACGCGCTTTCGCCACAGACCAATAGGATGGAGTCCGAGGCGGAGTTACCG 3720  
Db 3661 GCCAGTGTACGCGCTTTCGCCACAGACCAATAGGATGGAGTCCGAGGCGGAGTTACCG 3720  
QY 3721 GTGCCCCCGGAGCGGAACGGGATGACCAACAACTCCAGGCGACAACTATGCCCTG 3780  
Db 3721 GTGCCCCCGGAGCGGAACGGGATGACCAACAACTCCAGGCGACAACTATGCCCTG 3780  
QY 3781 GAGAACTACTATGATCTTCAACAGCAGCGCGGGAACCCGGGACCAACCGGCTACCTC 3840  
Db 3781 GAGAACTACTATGATCTTCAACAGCAGCGCGGGAACCCGGGACCAACCGGCTACCTC 3840  
QY 3841 GAGGCAACATGTCTCATCACGAGGAGCGAGACGCGCGGTGAACCGCTGGCGTAC 3900  
Db 3841 GAGGCAACATGTCTCATCACGAGGAGCGAGACGCGCGGTGAACCGCTGGCGTAC 3900  
QY 3901 AAGTGGCGGGCAGATGGCCACCAACAGAGTCCACCACTGCCCCCGGACCGGC 3960  
Db 3901 AAGTGGCGGGCAGATGGCCACCAACAGAGTCCACCACTGCCCCCGGACCGGC 3960  
QY 3961 ACCTTAACTCTCAGAAATCTGTCGCGGAGGTCGTTGGATGGAGGAGGAGTGTACTC 4020  
Db 3961 ACCTTAACTCTCAGAAATCTGTCGCGGAGGTCGTTGGATGGAGGAGGAGTGTACTC 4020  
QY 4021 CAAGGACCCATCTGGGCGCAAGATCCAGAGACGCGGGCGCACTTCAACCCCTCTCCGGCC 4080  
Db 4021 CAAGGACCCATCTGGGCGCAAGATCCAGAGACGCGGGCGCACTTCAACCCCTCTCCGGCC 4080  
QY 4081 ATGGGCGGATTCGGACTCAAAACCAACCGCCCATGATGCTCATCAAGAACCGCTGTG 4140  
Db 4081 ATGGGCGGATTCGGACTCAAAACCAACCGCCCATGATGCTCATCAAGAACCGCTGTG 4140  
QY 4141 CCGGAAATATCACAGCTTCTCGGAGGTCGCGTCAAGAGTTCATCAACCCAGTACAGC 4200  
Db 4141 CCGGAAATATCACAGCTTCTCGGAGGTCGCGTCAAGAGTTCATCAACCCAGTACAGC 4200  
QY 4201 ACCGGCAGGTCAACCTGGAGATGGAGTGGAGCTCAAGAGGAAACTCCAAGAGGTG 4260  
Db 4201 ACCGGCAGGTCAACCTGGAGATGGAGTGGAGCTCAAGAGGAAACTCCAAGAGGTG 4260  
QY 4261 AACCCAGAGATTCAGTACAAACAACTAAGAGCCCGGAGTTCGAGTTCGCGCCG 4320  
Db 4261 AACCCAGAGATTCAGTACAAACAACTAAGAGCCCGGAGTTCGAGTTCGCGCCG 4320  
QY 4321 GACGACCGGGGAAATACAGAACCCAGACCTATCGGAACCCGATACCTTACCCGACCC 4380  
Db 4321 GACGACCGGGGAAATACAGAACCCAGACCTATCGGAACCCGATACCTTACCCGACCC 4380  
QY 4381 CTTTAAACCCATTCATGTCGATACCTCAATAAACCGTGTATTCGTGTGTCAGTAAATACT 4440  
Db 4381 CTTTAAACCCATTCATGTCGATACCTCAATAAACCGTGTATTCGTGTGTCAGTAAATACT 4440



QY 1501 AACAGGTGGTGAATCCGCCAAGCCATCTCTGGGGGCTCAAAGGTGGGTGCTCATCAG 1560  
Db 1501 AACAGGTGGTGAATCCGCCAAGCCATCTCTGGGGGCTCAAAGGTGGGTGCTCATCAG 1560  
QY 1561 AAATGTAATCTCTGTTCAAAATGATTTACTACCCCTGTCTATGTAATCTTCAATCAAAAC 1620  
Db 1561 AAATGTAATCTCTGTTCAAAATGATTTACTACCCCTGTCTATGTAATCTTCAATCAAAAC 1620  
QY 1621 ATGTGTGTGGTGGATGGGAATTCACAGACTTTGAACACCAGCAGCCGCTGGAGGAC 1680  
Db 1621 ATGTGTGTGGTGGATGGGAATTCACAGACTTTGAACACCAGCAGCCGCTGGAGGAC 1680  
QY 1681 CGCATGTTCAAAATTTGAATCTGATTAAGCGGCTCCCGCAGATTTTGGCAAGATTACTAAG 1740  
Db 1681 CGCATGTTCAAAATTTGAATCTGATTAAGCGGCTCCCGCAGATTTTGGCAAGATTACTAAG 1740  
QY 1741 CAGGAAGTCAAGGACTTTTTTGTCTGGGCAAGGTCAATCAGGTGCGGTCAGTCAAG 1800  
Db 1741 CAGGAAGTCAAGGACTTTTTTGTCTGGGCAAGGTCAATCAGGTGCGGTCAGTCAAG 1800  
QY 1801 TTTAAAGTTCACAGGAATTCGCGGAATTAAGGGGCGGAGAAATCTCTAAAGCGCCCA 1860  
Db 1801 TTTAAAGTTCACAGGAATTCGCGGAATTAAGGGGCGGAGAAATCTCTAAAGCGCCCA 1860  
QY 1861 CTGGGTGACGTCACAATACTAGCTATAAAAGTCTGGAGAGCGGCGCAGCTCTCATTTT 1920  
Db 1861 CTGGGTGACGTCACAATACTAGCTATAAAAGTCTGGAGAGCGGCGCAGCTCTCATTTT 1920  
QY 1921 GTTCCCGAGAGCGCTCCGAGTTACAGCTGACTGTTGATCCGCTCCTCTCGAGCGGTC 1980  
Db 1921 GTTCCCGAGAGCGCTCCGAGTTACAGCTGACTGTTGATCCGCTCCTCTCGAGCGGTC 1980  
QY 1981 AATTGGAATTCAGGTATGATTTGCAAAATGTGACTATCATGCTCAATTTGACAAATTTCT 2040  
Db 1981 AATTGGAATTCAGGTATGATTTGCAAAATGTGACTATCATGCTCAATTTGACAAATTTCT 2040  
QY 2041 AACAAATGTGATGTAATTTGAAATCGGGGCAAAATGATGATCTGTCACAAT 2100  
Db 2041 AACAAATGTGATGTAATTTGAAATCGGGGCAAAATGATGATCTGTCACAAT 2100  
QY 2101 GTAACTCACTGTCAAAATTTGTCTAGGATTTCCCGCTGGGAAAGGAAATCTGTAGAT 2160  
Db 2101 GTAACTCACTGTCAAAATTTGTCTAGGATTTCCCGCTGGGAAAGGAAATCTGTAGAT 2160  
QY 2161 TTTGGGATTTGACGATGCAATAAAGAAACAGTAATAAAGCAGTAGTCAATCTCTTTT 2220  
Db 2161 TTTGGGATTTGACGATGCAATAAAGAAACAGTAATAAAGCAGTAGTCAATCTCTTTT 2220  
QY 2221 GTTGTACACCTCCAGATTGGTTGGAAAGAGTTGGTGAAGTCTTCCGAGTTTGTGGC 2280  
Db 2221 GTTGTACACCTCCAGATTGGTTGGAAAGAGTTGGTGAAGTCTTCCGAGTTTGTGGC 2280  
QY 2281 CTTGAAGCGGGCCACCGAAACCAAAACCAATCAGCAGCATCAAGATCAAGCCGTTGT 2340  
Db 2281 CTTGAAGCGGGCCACCGAAACCAAAACCAATCAGCAGCATCAAGATCAAGCCGTTGT 2340  
QY 2341 CTTGTGCTGCTGGTTATAACTATCTCGACCCGGAACCGTCTCGATCAGAGAGCCCT 2400  
Db 2341 CTTGTGCTGCTGGTTATAACTATCTCGACCCGGAACCGTCTCGATCAGAGAGCCCT 2400  
QY 2401 GTCAACAGGCGACAGAGGTGGCGGAGACGACGATCTCTGTAACAGCAGCAGTTGAG 2460  
Db 2401 GTCAACAGGCGACAGAGGTGGCGGAGACGACGATCTCTGTAACAGCAGCAGTTGAG 2460  
QY 2461 GCGGGAGACAACCCCTACCTCAAGTACACACCGCGAGCCCGGTTTCAAGGAGCTC 2520  
Db 2461 GCGGGAGACAACCCCTACCTCAAGTACACACCGCGAGCCCGGTTTCAAGGAGCTC 2520  
QY 2521 GCCGAGACACATCTTTCTGGGGGAAACCTCGGAAAGGCACTTTTCAAGGCAAGAAAGG 2580  
Db 2521 GCCGAGACACATCTTTCTGGGGGAAACCTCGGAAAGGCACTTTTCAAGGCAAGAAAGG 2580  
QY 2581 GTTCTCGAACCTTTTGGCTGTGTAAGAGGTGCTTAAGACGCGCCCTACCGGAAAGCGG 2640

Db 2581 GTTCTCGAACCTTTTGGCTGTGTAAGAGGTGCTTAAGACGCGCCCTACCGGAAAGCGG 2640  
QY 2641 ATAGACGACCACTTTTCCAAAAGAAAGAGCTCGGACCGAAGAGGACTTCCAAGCTTTCC 2700  
Db 2641 ATAGACGACCACTTTTCCAAAAGAAAGAGCTCGGACCGAAGAGGACTTCCAAGCTTTCC 2700  
QY 2701 ACCTCGTCAGACCGCGAAGCTTGGACCCAGCGGATCCAGCAGCTGCAAAATCCAGCCCAA 2760  
Db 2701 ACCTCGTCAGACCGCGAAGCTTGGACCCAGCGGATCCAGCAGCTGCAAAATCCAGCCCAA 2760  
QY 2761 CCAGCCTCAAGTTTGGGAGCTGATACAAATGCTCGGAGGTGGCGGCCAATGGGCGAC 2820  
Db 2761 CCAGCCTCAAGTTTGGGAGCTGATACAAATGCTCGGAGGTGGCGGCCAATGGGCGAC 2820  
QY 2821 AATAACCAAGTGGCGATGGAGTGGGCAATGCTCTGGGAGATTGGCAATTTGCAAG 2880  
Db 2821 AATAACCAAGTGGCGATGGAGTGGGCAATGCTCTGGGAGATTGGCAATTTGCAAG 2880  
QY 2881 TGGATGGGGACAGAGTCTGACCAAGTCCACCGAACCTTGGTGTCTGCCAGCTTCAAC 2940  
Db 2881 TGGATGGGGACAGAGTCTGACCAAGTCCACCGAACCTTGGTGTCTGCCAGCTTCAAC 2940  
QY 2941 AACCAACAGTACCCGAGAGATCAAAAGCGGCTCCGTTCGACGGAAGCAACGCGAAGCCTTAC 3000  
Db 2941 AACCAACAGTACCCGAGAGATCAAAAGCGGCTCCGTTCGACGGAAGCAACGCGAAGCCTTAC 3000  
QY 3001 TTTGGATACAGCACCCCTGGGGGTACTTTGACTTTAAACCGCTTCCACAGCCTGGAGC 3060  
Db 3001 TTTGGATACAGCACCCCTGGGGGTACTTTGACTTTAAACCGCTTCCACAGCCTGGAGC 3060  
QY 3061 CCCGAGACTGGGAAAGACTCATCAACAACTACTGGGGCTTCAGACCCCGTCTCCTCAGA 3120  
Db 3061 CCCGAGACTGGGAAAGACTCATCAACAACTACTGGGGCTTCAGACCCCGTCTCCTCAGA 3120  
QY 3121 GTCAAAATCTTCAACATTTCAAGTCAAAAGAGTCAACGCTGACGAGTCCACACCAACCATC 3180  
Db 3121 GTCAAAATCTTCAACATTTCAAGTCAAAAGAGTCAACGCTGACGAGTCCACACCAACCATC 3180  
QY 3181 GCACAACCTCTACCTCCACCGTCCAAAGTGTTTACCGACGACGACTACAGCTGCCCTAC 3240  
Db 3181 GCACAACCTCTACCTCCACCGTCCAAAGTGTTTACCGACGACGACTACAGCTGCCCTAC 3240  
QY 3241 GTCTGCGCAACCGGACCGGAGGATGCTCGCGGCTTCCCTCGGAGGTCTTTACGCTG 3300  
Db 3241 GTCTGCGCAACCGGACCGGAGGATGCTCGCGGCTTCCCTCGGAGGTCTTTACGCTG 3300  
QY 3301 CCGCAGTACCGTTTACCGCAGCTGAAACCGGCAACACACAGAAATCCACCGAGAGGAGC 3360  
Db 3301 CCGCAGTACCGTTTACCGCAGCTGAAACCGGCAACACACAGAAATCCACCGAGAGGAGC 3360  
QY 3361 AGCTTCTTCTGCTAGATGATCTTTCCAGCAAGATGCTGAGAACGCGCAACAACTTTGAG 3420  
Db 3361 AGCTTCTTCTGCTAGATGATCTTTCCAGCAAGATGCTGAGAACGCGCAACAACTTTGAG 3420  
QY 3421 TTTTACTTACAATCTTTCAGGAGGTGCTTCCACTCCAGCTTCCCTCCAGTCAAGACCTG 3480  
Db 3421 TTTTACTTACAATCTTTCAGGAGGTGCTTCCACTCCAGCTTCCCTCCAGTCAAGACCTG 3480  
QY 3481 TTTCAAGTGGCCCAACCCGCTGGTGGACCACTTGTACCGCTTCTGTAGACAAATAAC 3540  
Db 3481 TTTCAAGTGGCCCAACCCGCTGGTGGACCACTTGTACCGCTTCTGTAGACAAATAAC 3540  
QY 3541 ACTGGCGAGTCCAGTTCAACAAAGACCTTGGCGGAGATACGCCAACCTTCAAAAAAC 3600  
Db 3541 ACTGGCGAGTCCAGTTCAACAAAGACCTTGGCGGAGATACGCCAACCTTCAAAAAAC 3600  
QY 3601 TGGTTCCCGGGCCCATGGCCGAGCCAGGGCTGGAACTTGGGCTTCGGGGTCAACCGC 3660  
Db 3601 TGGTTCCCGGGCCCATGGCCGAGCCAGGGCTGGAACTTGGGCTTCGGGGTCAACCGC 3660  
QY 3661 GCCAGTGTCAAGCGCTTTCGCCACGACCAATAGATCGAGCTCGAGGCGGAGTTACCG 3720





QY 66 AGCTGCCAGACGCGGCTCTGGCGTCCGCCGCCAAACGAGCGAGCGAGCGAA 125  
Db 61 AGCTGCCAGACGCGGCTCTGGCGTCCGCCGCCAAACGAGCGAGCGAGCGAA 120  
QY 126 CGCGACAGGGGAGAGTCCACACTCTCAAGCAGAGGGGTTTGTAGCAGTGAATGCA 185  
Db 121 CGCGACAGGGGAGAGTCCACACTCTCAAGCAGAGGGGTTTGTAGCAGTGAATGCA 180  
QY 186 TAATGATGTAATGCTTATGTCACGATAGTAAATGATTAACAGTCAATGATGTTT 245  
Db 181 TAATGATGTAATGCTTATGTCACGATAGTAAATGATTAACAGTCAATGATGTTT 240  
QY 246 TATCCAAATAGGAAGAAAGCGCGTATGAGTCTCGGAGACTTCCGGGGTATAAAGAC 305  
Db 241 TATCCAAATAGGAAGAAAGCGCGTATGAGTCTCGGAGACTTCCGGGGTATAAAGAC 300  
QY 306 CGAGTGAACGAGCCCGCGCATCTTTGCTGAGTCTGAGTCTGAGGAGCTCGCTGCCAT 365  
Db 301 CGAGTGAACGAGCCCGCGCATCTTTGCTGAGTCTGAGTCTGAGGAGCTCGCTGCCAT 360  
QY 366 GGCTACCTTCTATGAAGTCAATGTTTCGGCTCCCATTTGACGTGAGGAACATCTGCCCTGG 425  
Db 361 GGCTACCTTCTATGAAGTCAATGTTTCGGCTCCCATTTGACGTGAGGAACATCTGCCCTGG 420  
QY 426 AATTTCTGACAGCTTTGAGTCTGGTAACTGGTCAAAATTTGGAGTGCCTCCAGATC 485  
Db 421 AATTTCTGACAGCTTTGAGTCTGGTAACTGGTCAAAATTTGGAGTGCCTCCAGATC 480  
QY 486 AGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGCATAGAAATTCGCCG 545  
Db 481 AGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGCATAGAAATTCGCCG 540  
QY 546 CGTGTCTCTGACAGTGAACAAATTTTCCAGCAGAGTCCAAATTTCTTTGGCAGTT 605  
Db 541 CGTGTCTCTGACAGTGAACAAATTTTCCAGCAGAGTCCAAATTTCTTTGGCAGTT 600  
QY 606 TGAAGAGGATCGAATATTTTCTATCTGACACGCTTGTGGAGACCTCCGCACTCTTC 665  
Db 601 TGAAGAGGATCGAATATTTTCTATCTGACACGCTTGTGGAGACCTCCGCACTCTTC 660  
QY 666 CATGGTCTCGCGCTGACGTGAGTCAAGTTCCGCCAGCTGGTGAAGTGTCTTCCA 725  
Db 661 CATGGTCTCGCGCTGACGTGAGTCAAGTTCCGCCAGCTGGTGAAGTGTCTTCCA 720  
QY 726 GGAATTTGAACCCAGATCAACGACTGGGTGGCTGCGCATCAACAGGTAAAGAGGCGGAGC 785  
Db 721 GGAATTTGAACCCAGATCAACGACTGGGTGGCTGCGCATCAACAGGTAAAGAGGCGGAGC 780  
QY 786 CAATAAGGTGGTGGATCTGGGTATATTCGGCTACCTGCTCGGAGGTCCAAACCGGA 845  
Db 781 CAATAAGGTGGTGGATCTGGGTATATTCGGCTACCTGCTCGGAGGTCCAAACCGGA 840  
QY 846 GCTTCAGTGGGCTGACAAACCTGGACAGTATAAATTTGGCGCCCTGAACTGGAGGA 905  
Db 841 GCTTCAGTGGGCTGACAAACCTGGACAGTATAAATTTGGCGCCCTGAACTGGAGGA 900  
QY 906 GGCAGAACGCTCGTCCGCGAGTTTCTGGCAGAAATCCTCGCAGCGCTCGCAGGAGCGGC 965  
Db 901 GGCAGAACGCTCGTCCGCGAGTTTCTGGCAGAAATCCTCGCAGCGCTCGCAGGAGCGGC 960  
QY 966 TTTCCAGCGGTGAGTTCTCGCTGACCGGTATCAAAAGAGACTTCCAGAAATACAT 1025  
Db 961 TTTCCAGCGGTGAGTTCTCGCTGACCGGTATCAAAAGAGACTTCCAGAAATACAT 1020  
QY 1026 GCGGCTCGTCAACTGCTGGAGCAGCGCATCACTTCGAGAACAGTGGATCCAGGA 1085  
Db 1021 GCGGCTCGTCAACTGCTGGAGCAGCGCATCACTTCGAGAACAGTGGATCCAGGA 1080  
QY 1086 AAATCAGGAGAGTACCTCTCTTCACTCCACCGGCAACTCTCGAGCGAGTCAAGGC 1145  
Db 1081 AAATCAGGAGAGTACCTCTCTTCACTCCACCGGCAACTCTCGAGCGAGTCAAGGC 1140  
QY 1146 CCGCTCGCAACGCGACCAAAATTAATGAGTCTGACAAAAGCGCGGTGACTACCTCGT 1205

Db 1141 CGCGTCTGACAAACGCGACCAAAATTAATGAGTCTGACAAAAGCGGTGAGTACCTCGT 1200  
QY 1206 GGGAGCTCCGTTCCGAGGACATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGTAA 1265  
Db 1201 GGGAGCTCCGTTCCGAGGACATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGTAA 1260  
QY 1266 TGGCTACGACCCGGCTACGCGGATCCATCTCTACGCTGGTGTGACGCTCTCTCAA 1325  
Db 1261 TGGCTACGACCCGGCTACGCGGATCCATCTCTACGCTGGTGTGACGCTCTCTCAA 1320  
QY 1326 CAAGAGAACACCGTCTGGCTACGAGCCGCCACGACCGGCAAGACCAACATCGCGGA 1385  
Db 1321 CAAGAGAACACCGTCTGGCTACGAGCCGCCACGACCGGCAAGACCAACATCGCGGA 1380  
QY 1386 GGCATCGCCACACACTGTGCCCTTTTACGGCTGGGTGAACATGGACCAATGAAACTTTCC 1445  
Db 1381 GGCATCGCCACACACTGTGCCCTTTTACGGCTGGGTGAACATGGACCAATGAAACTTTCC 1440  
QY 1446 CTTTAAATGACTGTGGACAAAATGCTCATTTGGTGGAGGAGGAAAGATGACCAACAA 1505  
Db 1441 CTTTAAATGACTGTGGACAAAATGCTCATTTGGTGGAGGAGGAAAGATGACCAACAA 1500  
QY 1506 GGTGTTGAAATCCGCCAAGGCCATCTGGGGGCTCAAGSTGCGGTGCGATCAGAAATG 1565  
Db 1501 GGTGTTGAAATCCGCCAAGGCCATCTGGGGGCTCAAGSTGCGGTGCGATCAGAAATG 1560  
QY 1566 TAAATCTCTGTTCAAAATGATTTCTACCCCTGTCAATGTAACCTTCCCAATACAAACATGTG 1625  
Db 1561 TAAATCTCTGTTCAAAATGATTTCTACCCCTGTCAATGTAACCTTCCCAATACAAACATGTG 1620  
QY 1626 TGTGTTGATGAGTGGGAATTTCCAGCACTTTGAACACACAGCAGCCGCTGGAGGACCGCAT 1685  
Db 1621 TGTGTTGATGAGTGGGAATTTCCAGCACTTTGAACACACAGCAGCCGCTGGAGGACCGCAT 1680  
QY 1686 GTTCAAAATTTGAATGACTAAGCGGCTCCCGCAGATTTTGGCAAGATTAATTAAGAGGA 1745  
Db 1681 GTTCAAAATTTGAATGACTAAGCGGCTCCCGCAGATTTTGGCAAGATTAATTAAGAGGA 1740  
QY 1746 AGTCAAGGACTTTTTTTGTTGGCAAAAGTCAATCAGGTCCCGTGAATCAGGAGTTTAA 1805  
Db 1741 AGTCAAGGACTTTTTTTGTTGGCAAAAGTCAATCAGGTCCCGTGAATCAGGAGTTTAA 1800  
QY 1806 AGTTCGAGGAAATTTGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCACCTGGG 1865  
Db 1801 AGTTCGAGGAAATTTGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCACCTGGG 1860  
QY 1866 TGACGTCAACCAATACCTAGCTATATAAAGTCTGGAGAGCGGCGCAGGCTCTCATTTGTTCC 1925  
Db 1861 TGACGTCAACCAATACCTAGCTATATAAAGTCTGGAGAGCGGCGCAGGCTCTCATTTGTTCC 1920  
QY 1926 CGAGACGCTCGCAGTTTCAGACGTGACTGTTGATCCCGCTCTCTCGCAGCGCTCAATTG 1985  
Db 1921 CGAGACGCTCGCAGTTTCAGACGTGACTGTTGATCCCGCTCTCTCGCAGCGCTCAATTG 1980  
QY 1986 GAATTCAGGTATGATGCAAAATGAGTATCATGCTCAATTTGACAAATTTCTAACAA 2045  
Db 1981 GAATTCAGGTATGATGCAAAATGAGTATCATGCTCAATTTGACAAATTTCTAACAA 2040  
QY 2046 ATGTGATGATGATGATAATTTGAAATCGGGGCAAAATGAGTATCTGTCAAAATGAAAC 2105  
Db 2041 ATGTGATGATGATGATAATTTGAAATCGGGGCAAAATGAGTATCTGTCAAAATGAAAC 2100  
QY 2106 TCACGTCAAAATTTGTCTGGGATTTCCCGCTGGGAAAGGAAACTTGTGAGATTTGG 2165  
Db 2101 TCACGTCAAAATTTGTCTGGGATTTCCCGCTGGGAAAGGAAACTTGTGAGATTTGG 2160  
QY 2166 GGAATTTGACGATGCAATTAAGAAACAGTAAATAAGCGAGTAGTCAATCTTTTGTGA 2225  
Db 2161 GGAATTTGACGATGCAATTAAGAAACAGTAAATAAGCGAGTAGTCAATCTTTTGTGA 2220  
QY 2226 TCACCTCCAGATGTTTGGAGAAAGTTGGTGAAGTCTTCGCGAGTTTGGGCTTGA 2285







QY 786 CAATAAGGTGGTGGATTCTGGGTATATTCCTCGGCTTACCTGTGCGGAAGGTCCAAACCGGA 845  
Db 661 CAATAAGGTGGTGGATTCTGGGTATATTCCTCGGCTTACCTGTGCGGAAGGTCCAAACCGGA 720  
QY 846 GCTTCAGTGGGCGTGGACAAACCTCGGACGAGTATAAATTGGCCGCCCTGAAATCTGGAGGA 905  
Db 721 GCTTCAGTGGGCGTGGACAAACCTCGGACGAGTATAAATTGGCCGCCCTGAAATCTGGAGGA 780  
QY 906 GCGCAACCGCTGCTGGCGGAGTTCCTGGCAGAAATCTTCGACAGCCTCGCAGGAGGCGGC 965  
Db 781 GCGCAACCGCTGCTGGCGGAGTTCCTGGCAGAAATCTTCGACAGCCTCGCAGGAGGCGGC 840  
QY 966 TTCGAGCGTGAATTCGGCTGACCGGTCATCAAAAGCAGAGCTTCCACAGAAATACAT 1025  
Db 841 TTCGAGCGTGAATTCGGCTGACCGGTCATCAAAAGCAGAGCTTCCACAGAAATACAT 900  
QY 1026 GCGCTGCTCAACTGGCTCGTGAGCAGGCATCACTTCCGAGAAGCAGTGGATCCAGGA 1085  
Db 901 GCGCTGCTCAACTGGCTCGTGAGCAGGCATCACTTCCGAGAAGCAGTGGATCCAGGA 960  
QY 1086 AAATCAGGAGACTACTCTCTTCAACTCCACCGCACTCTCGGAGCCAGATCAAGGC 1145  
Db 961 AAATCAGGAGACTACTCTCTTCAACTCCACCGCACTCTCGGAGCCAGATCAAGGC 1020  
QY 1146 GCGCTGCAACGCGGACCAAAATATGAGTCTGACAAAAGCGGGTGGACTACTCTGT 1205  
Db 1021 GCGCTGCAACGCGGACCAAAATATGAGTCTGACAAAAGCGGGTGGACTACTCTGT 1080  
QY 1206 GGGGAGCTCCGTTCCCGAGGACATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGTAA 1265  
Db 1081 GGGGAGCTCCGTTCCCGAGGACATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGTAA 1140  
QY 1266 TGGCTACGACCGGCTACCGGGATCACTCTTACGGCTGGTGTACGGCTCTTCAA 1325  
Db 1141 TGGCTACGACCGGCTACCGGGATCACTCTTACGGCTGGTGTACGGCTCTTCAA 1200  
QY 1326 CAAGAGGAACACGCTCTGCTCTACGACCCGCGACCGGCAAGACCAACATCGCGGA 1385  
Db 1201 CAAGAGGAACACGCTCTGCTCTACGACCCGCGACCGGCAAGACCAACATCGCGGA 1260  
QY 1386 GGCATCGCCACACTGTGCCCTTTTACGGCTGCGTGAATCTGGACCAATGAAATTTTCC 1445  
Db 1261 GGCATCGCCACACTGTGCCCTTTTACGGCTGCGTGAATCTGGACCAATGAAATTTTCC 1320  
QY 1446 CTTTAATGACTGTGCAAAAATGCTCATTTGGTGGGAGGAGGAAGATGACCAACAA 1505  
Db 1321 CTTTAATGACTGTGCAAAAATGCTCATTTGGTGGGAGGAGGAAGATGACCAACAA 1380  
QY 1506 GGTGGTTGAATCGCCCAAGGCCATCTGGGGGCTCAAAGGTGCGGGTGCATCAGAAATG 1565  
Db 1381 GGTGGTTGAATCGCCCAAGGCCATCTGGGGGCTCAAAGGTGCGGGTGCATCAGAAATG 1440  
QY 1566 TAAATCCTCTGTTCAAATGATTCTACCCCTGTCAATTTGTAATCTTCAATCAAAATGTTG 1625  
Db 1441 TAAATCCTCTGTTCAAATGATTCTACCCCTGTCAATTTGTAATCTTCAATCAAAATGTTG 1500  
QY 1626 TGTGGTGGTGGATTTCCAGACCTTTGACACCCAGCAGCCGCTGGAGACCGCAT 1685  
Db 1501 TGTGGTGGTGGATTTCCAGACCTTTGACACCCAGCAGCCGCTGGAGACCGCAT 1560  
QY 1686 GTTCAAATTTGAATGACTAAGCGGCTCCCGCCAGATTTTGGCAAGATTACTAAGCAGGA 1745  
Db 1561 GTTCAAATTTGAATGACTAAGCGGCTCCCGCCAGATTTTGGCAAGATTACTAAGCAGGA 1620  
QY 1746 AGTCAAGGACTTTTGTCTGGGCAAGGTCAATCAGTGGCCGCTGACTCAGATTTAA 1805  
Db 1621 AGTCAAGGACTTTTGTCTGGGCAAGGTCAATCAGTGGCCGCTGACTCAGATTTAA 1680  
QY 1806 AGTTCACGAGAAATGGCGGAACTAAAGGGCGGAGAAATCTTAAAGCGCCACTGGG 1865  
Db 1681 AGTTCACGAGAAATGGCGGAACTAAAGGGCGGAGAAATCTTAAAGCGCCACTGGG 1740

QY 1866 TGACGTCCAAATACTAGCTATAAAGTCTGGAGAACGGGGCCAGGCTCTCATTTGTTCC 1925  
Db 1741 TGACGTCCAAATACTAGCTATAAAGTCTGGAGAACGGGGCCAGGCTCTCATTTGTTCC 1800  
QY 1926 CGAGCGCTCGAGTTCAGACGTGACTTGTGTATCCGCTCTCTGCGACCGCTCAATG 1985  
Db 1801 CGAGCGCTCGAGTTCAGACGTGACTTGTGTATCCGCTCTCTGCGACCGCTCAATG 1860  
QY 1986 GAAATCAAGGTATGATTCGAAATGTGACTATCATGCTCAATTTGCAACATTTCTTAA 2045  
Db 1861 GAAATCAAGGTATGATTCGAAATGTGACTATCATGCTCAATTTGCAACATTTCTTAA 1920  
QY 2046 ATGTGATGAATGTGAATTTGAATTCGGGGCAAAATGATGATGATCTGTCACATGTAAC 2105  
Db 1921 ATGTGATGAATGTGAATTTGAATTCGGGGCAAAATGATGATGATCTGTCACATGTAAC 1980  
QY 2106 TCACGTCAAAATTTGTCATGGGATTCCTCGGAAAAGGAAAATTTGTGAGATTTGG 2165  
Db 1981 TCACGTCAAAATTTGTCATGGGATTTCCCTCGGAAAAGGAAAATTTGTGAGATTTGG 2040  
QY 2166 GGAATTTGACGATGCAATTAAGAACAGTAATAAAGCGAGTAGTCAATGCTTTTGTGA 2225  
Db 2041 GGAATTTGACGATGCAATTAAGAACAGTAATAAAGCGAGTAGTCAATGCTTTTGTGA 2100  
QY 2226 TCACCTCCAGATTTGGTTGGAAGAAGTTGTTGAAGTCTTCGCGAGTTTGGGCTTGA 2285  
Db 2101 TCACCTCCAGATTTGGTTGGAAGAAGTTGTTGAAGTCTTCGCGAGTTTGGGCTTGA 2160  
QY 2286 AGCGGGCCACCGAAACCAATCAGCAGCATCAAGATCAAGCCCGTGTCTTGT 2345  
Db 2161 AGCGGGCCACCGAAACCAATCAGCAGCATCAAGATCAAGCCCGTGTCTTGT 2220  
QY 2346 GCTGCTGTTATAACTATCTCGGACCCGGAACCGTCTCGATCAGGAGAGCCTGTCAA 2405  
Db 2221 GCTGCTGTTATAACTATCTCGGACCCGGAACCGTCTCGATCAGGAGAGCCTGTCAA 2280  
QY 2406 CAGGGAGACGAGGTGCGCGAGAGCAGCATCTGTCACAGCAGCAGCTTGGCGGG 2465  
Db 2281 CAGGGAGACGAGGTGCGCGAGAGCAGCATCTGTCACAGCAGCAGCTTGGCGGG 2340  
QY 2466 AGACAACCTTACCTCAAGTACAAACCGCGACCGCGAGTTTCAGGAGAAAGCTCCCGGA 2525  
Db 2341 AGACAACCTTACCTCAAGTACAAACCGCGACCGCGAGTTTCAGGAGAAAGCTCCCGGA 2400  
QY 2526 CGACACATCTTTCGGGGGAAACCTCGGAAAGCAGTCTTTTCAGGCAAGAAAGGTTCT 2585  
Db 2401 CGACACATCTTTCGGGGGAAACCTCGGAAAGCAGTCTTTTCAGGCAAGAAAGGTTCT 2460  
QY 2586 CGAACCTTTTGGCTGTTGAAGAGGTGCTAAGACGGCCCTACCGGAAGCGGATAGA 2645  
Db 2461 CGAACCTTTTGGCTGTTGAAGAGGTGCTAAGACGGCCCTACCGGAAGCGGATAGA 2520  
QY 2646 CGACACATTTTCCAAAAGGAAAGAGGCTCGGACCGAAGAGGACTTCAACGCTTCCA 2705  
Db 2521 CGACACATTTTCCAAAAGGAAAGAGGCTCGGACCGAAGAGGACTTCAACGCTTCCA 2580  
QY 2706 GTCAGACGCGGAGCTGGACCCAGCGGATCCAGCAGCTGCAAAATCCGACGCCCAACG 2765  
Db 2581 GTCAGACGCGGAGCTGGACCCAGCGGATCCAGCAGCTGCAAAATCCGACGCCCAACG 2640  
QY 2766 CTCAGTTTGGAGCTGATACATGCTCGGGAGGTGGGCCCATTTGGGCGACATAA 2825  
Db 2641 CTCAGTTTGGAGCTGATACATGCTCGGGAGGTGGGCCCATTTGGGCGACATAA 2700  
QY 2826 CCAAGTTCGAGTGGAGTGGGCAATGCTCGGAGATTGGCATTTGGATTTCAACGTTGAT 2885  
Db 2701 CCAAGTTCGAGTGGAGTGGGCAATGCTCGGAGATTGGCATTTGGATTTCAACGTTGAT 2760  
QY 2886 GGGGACAGAGTCTGTCACCAAGTCCAGCGGACTCGGCTGCTGCCAGCTTACACACCA 2945  
Db 2761 GGGGACAGAGTCTGTCACCAAGTCCAGCGGACTCGGCTGCTGCCAGCTTACACACCA 2820  
QY 2946 CCAGTCCGAGAGATCAAAAGCGGCTCGTTCGACGGAAGCAACGCCAAACGCTACTTTGG 3005

Db 2821 CCGATACCGAGATCAAAAGCGCTCGTCCAGCGAAGCAACGCCAAGCGCTACTTTGG 2880  
QY 3006 ATACAGACACCCCTGGGGTACTTTGACTTTAAACGGCTTCACAGCACCTGGAGCCCGG 3065  
Db 2881 ATACAGACACCCCTGGGGTACTTTGACTTTAAACGGCTTCACAGCACCTGGAGCCCGG 2940  
QY 3066 AGACTGCAAGAGTCTATCAACAACTACTGGGGCTTCAGACCCCGGTCCCTCAGAGTCAA 3125  
Db 2941 AGACTGCAAGAGTCTATCAACAACTACTGGGGCTTCAGACCCCGGTCCCTCAGAGTCAA 3000  
QY 3126 AATCTTCAATTAAGTCAAGAGGTCAAGGTGCAAGGTTCACACCAACCATTCGCCAA 3185  
Db 3001 AATCTTCAATTAAGTCAAGAGGTCAAGGTGCAAGGTTCACACCAACCATTCGCCAA 3060  
QY 3186 CAACCTCACCTCCACCGTCCAGGTGTTTACGAGGAGGACTTACAGCTGCCCTACGTCGT 3245  
Db 3061 CAACCTCACCTCCACCGTCCAGGTGTTTACGAGGAGGACTTACAGCTGCCCTACGTCGT 3120  
QY 3246 CGGCAACCGGACCGAGGATGCTTCCCGGGCTTCCCTCCGAGGTCTTTTACGCTGCCGCA 3305  
Db 3121 CGGCAACCGGACCGAGGATGCTTCCCGGGCTTCCCTCCGAGGTCTTTTACGCTGCCGCA 3180  
QY 3306 GTACGGTTACGAGCGGTGAACCGCGCAACAACAGAAATAATCCCAACGAGAGGAGCGCTT 3365  
Db 3181 GTACGGTTACGAGCGGTGAACCGCGCAACAACAGAAATAATCCCAACGAGAGGAGCGCTT 3240  
QY 3366 CTTCGCTGAGTACTTCCCGAGAGAGTCTGAGAACGGGCAACAACCTTTGAGTTTAC 3425  
Db 3241 CTTCGCTGAGTACTTCCCGAGAGAGTCTGAGAACGGGCAACAACCTTTGAGTTTAC 3300  
QY 3426 CTACAACTTTGAGAGGTGCTTCCACTCCAGTCTCGCTCCCACTCAGAACCTGTTCAA 3485  
Db 3301 CTACAACTTTGAGAGGTGCTTCCACTCCAGTCTCGCTCCCACTCAGAACCTTTCAA 3360  
QY 3486 GCTGGCCCAACCCGCTGGTGACCACTGTTGTACCGCTTCGTGAGCAACAATAACACTGG 3545  
Db 3361 GCTGGCCCAACCCGCTGGTGACCACTGTTGTACCGCTTCGTGAGCAACAATAACACTGG 3420  
QY 3546 CGGAGTCCAGTTCACAAAGAACCTTCCCGGAGATAGCCCAACACCTTACAAAACCTGTT 3605  
Db 3421 CGGAGTCCAGTTCACAAAGAACCTTCCCGGAGATAGCCCAACACCTTACAAAACCTGTT 3480  
QY 3606 CCGGGGCCCACATGGCGCGCAACCCAGAGCTGGAACCTTGGGCTCCGGGTCAACCGCGCCAG 3665  
Db 3481 CCGGGGCCCACATGGCGCGCAACCCAGAGCTGGAACCTTGGGCTCCGGGTCAACCGCGCCAG 3540  
QY 3666 TGTTCAGGCTTCCCGACGACCAATAGATGGAGTTCGAGGGCGGAGTTACAGGTGCC 3725  
Db 3541 TGTTCAGGCTTCCCGACGACCAATAGATGGAGTTCGAGGGCGGAGTTACAGGTGCC 3600  
QY 3726 CCGCAGCGCAACCGCATGACCAACCACTCCAGGCGCAGCAACCTTACCTCGCTGGAGA 3785  
Db 3601 CCGCAGCGCAACCGCATGACCAACCACTCCAGGCGCAGCAACCTTACCTCGCTGGAGA 3660  
QY 3786 CACTATGATCTTCAACAGCGCAGCGCGCAACCCGGGCAACCCCGCACCTTACCTCGAGGG 3845  
Db 3661 CACTATGATCTTCAACAGCGCAGCGCGCAACCCGGGCAACCCCGCACCTTACCTCGAGGG 3720  
QY 3846 CAACTGCTCATCAGAGGAGCGAGCGAGCGAGCGAGCGGTGAACCGCGTGCCTGACACGT 3905  
Db 3721 CAACTGCTCATCAGAGGAGCGAGCGAGCGAGCGAGCGGTGAACCGCGTGCCTGACACGT 3780  
QY 3906 CGCGGGCAGATGCGCACCAACCAACAGAGCTCCACCTTCCGCTGCCCGCACCGGACGTA 3965  
Db 3781 CGCGGGCAGATGCGCACCAACCAACAGAGCTCCACCTTCCGCTGCCCGCACCGGACGTA 3840  
QY 3966 CAACTCCAGGAATCGTGCCTGCCCGCAGCGGTGATGGAGAGGAGCGGTGACCTCCAGG 4025  
Db 3841 CAACTCCAGGAATCGTGCCTGCCCGCAGCGGTGATGGAGAGGAGCGGTGACCTCCAGG 3900  
QY 4026 ACCATCTGGGCAAGATCCCAAGAGCGGGGCGCACTTTCACCCCTCTCCGCGCATGGG 4085

Db 3901 ACCCATCTGGGCCAAGATCCAGAGACGGGGCGCACTTTACCCCTCTCGGCCATGGG 3960  
QY 4086 CGGATTCGAGTCAAAACACCCACCGCCCATGATGCTCATCAAGAACACGCTGTGCGCGG 4145  
Db 3961 CGGATTCGAGTCAAAACACCCACCGCCCATGATGCTCATCAAGAACACGCTGTGCGCGG 4020  
QY 4146 AATATATCACAGCTTCTCGGACGTCGCGGTCCAGAGCTTATCATCACAGTACAGACCGG 4205  
Db 4021 AATATATCACAGCTTCTCGGACGTCGCGGTCCAGAGCTTATCATCACAGTACAGACCGG 4080  
QY 4206 GCAGGTCAACCGTGGAGATGGAGTGGGAGCTCAAGAGGAACTCCAGAGGTGGAACCC 4265  
Db 4081 GCAGGTCAACCGTGGAGATGGAGTGGGAGCTCAAGAGGAACTCCAGAGGTGGAACCC 4140  
QY 4266 AGAGATCCAGTACAAAAAACAATCAACGACCCCGAGTTTGTGGACTTTGCCCGGACAG 4325  
Db 4141 AGAGATCCAGTACAAAAAACAATCAACGACCCCGAGTTTGTGGACTTTGCCCGGACAG 4200  
QY 4326 CACCGGGGAATACAGAACCAACCACTATCGGACCCGATCTTACCCGACCCCTTTA 4385  
Db 4201 CACCGGGGAATACAGAACCAACCACTATCGGACCCGATCTTACCCGACCCCTTTA 4260  
QY 4386 ACCCATTCATGCGCATACCTCAATAAACCGGTGATTTCGTGTCAGTAAATACTGCCTC 4445  
Db 4261 ACCCATTCATGCGCATACCTCAATAAACCGGTGATTTCGTGTCAGTAAATACTGCCTC 4320  
QY 4446 TTGTGTCATTCATGATTAACAGCTTACAACTATCAAAAACCTCTCTGTTGAGAGTG 4505  
Db 4321 TTGTGTCATTCATGATTAACAGCTTACAACTATCAAAAACCTCTCTGTTGAGAGTG 4380  
QY 4506 TGGCACTCTCCCGCTGTCGCG 4527  
Db 4381 TGGCACTCTCCCGCTGTCGCG 4402

## RESULT 5

AY388617

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

AY388617 4693 bp DNA circular VRL 25-MAY-2004  
Bovine adeno-associated virus, complete genome.  
AY388617.1 GI:38679253  
Bovine adeno-associated virus  
Bovine adeno-associated virus  
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Dependovirus.  
1 (bases 1 to 4693)  
Schmidt, M., Katano, H., Bossis, I. and Chiorini, J. A.  
Cloning and Characterization of a Bovine Adeno-Associated Virus  
J. Virol. 78 (12), 6509-6516 (2004)  
2 (bases 1 to 4693)  
Schmidt, M., Bossis, I. and Chiorini, J. A.  
Direct Submission  
Submitted (11-SEP-2003) NIDCR, NIH, 9000 Rockville Pike 10/1N112,  
Bethesda, MD 20892, USA  
Location/Qualifiers  
1. 4693  
/organism="Bovine adeno-associated virus"  
/mol\_type="genomic DNA"  
/isolation\_source="Bovine adenovirus 2 culture AtCC  
VR-314"  
/db\_xref="taxon:256548"  
368..2200  
/gene="rep"  
368..2200  
/gene="rep"  
/codon\_start=1  
/product="Rep"  
/protein\_id="AAR26464.1"  
/db\_xref="GI:38679254"  
gene  
CDS

[illegible]

QY 1678 GACCGGATGTTCAAAATTTGAATGAACTAAGCGGCTCCCGCAGATTTTGGCAAGATTACT 1737  
 Db 1682 GACCGGATGTTCAAGATTTGAATGAACTAAGCGGCTCCCGCAGATTTTGGCAAGATTACT 1741  
 QY 1738 AAGCAGGAGTCAAGGACTTTTGGTGGGCAAAAGGTCAATCAGGTGCGGCTGACTCAC 1797  
 Db 1742 AAGCAGGAGTCAAGGACTTTTGGTGGGCAAAAGGTCAATCAGGTGCGGCTGACTCAC 1801  
 QY 1798 GAGTTTAAAGTTCCAGGGAATTTGGCGGAATTAAGGGGCGGGAATTTCTAAAGCGC 1857  
 Db 1802 GAGTTTAAAGTTCCAGGGAATTTGGCGGAATTAAGGGGCGGGAATTTCTAAAGCGC 1861  
 QY 1858 CCACTGGGTGAGTCAACCAATTAAGTCTATAAAGTCTGGGAAGCGGCGCAGGCTCTCA 1917  
 Db 1862 CCACTGGGTGAGTCAACCAATTAAGTCTATAAAGTCTGGGAAGCGGCGCAGGCTCTCA 1921  
 QY 1918 TTTGTTCCCGAGAGCGCTCGAGTTTCAAGCTGATCTGATGCTGATGCTGCTCTGCGACG 1977  
 Db 1922 GTTGTCTCGAGAGCGCTCGAGTTTCAAGCTGATCTGATGCTGATGCTGCTCTGCGAC 1981  
 QY 1978 CTCAATTTGAATTTCAAGTATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2037  
 Db 1982 CTCAATTTGAATTTCAAGTATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2041  
 QY 2038 TCTTAACAAATGATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAAT 2097  
 Db 2042 ACGGGGAATTTGACGAGTGTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2101  
 QY 2098 AATGTAATCTACTCTCAATTTGATGAGTTTCAAGCTGATCTGATGCTGATGCTGATGCT 2157  
 Db 2102 AATGTAATCTACTCTCAATTTGATGAGTTTCAAGCTGATCTGATGCTGATGCTGATGCT 2161  
 QY 2158 GATTTTGGGATTTTGAAGTATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2217  
 Db 2162 GATTTTGAATTTGATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2221  
 QY 2218 TTTGTTGATCACTCTCAAGTATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2277  
 Db 2222 TTTGTTGATCACTCTCAAGTATGATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2281  
 QY 2278 GGCCTTCAAGCGGCGCCACCGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2337  
 Db 2282 GGCCTTCAAGCGGCGCCACCGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 2341  
 QY 2338 GGTCTTGTGCTGCTGATTTAATCTATCTCGACCCGGAATTTGAATTTGAATTTGAATTTGA 2397  
 Db 2342 GGTCTTGTGCTGCTGATTTAATCTATCTCGACCCGGAATTTGAATTTGAATTTGAATTTGA 2401  
 QY 2398 CTTGTCAAGGCGAGCGGTTGCGGAGAGCAAGATCTCTGATCAAGAGCAGCTT 2457  
 Db 2402 CTTGTCAAGGCGAGCGGTTGCGGAGAGCAAGATCTCTGATCAAGAGCAGCTT 2461  
 QY 2458 GAGCGGAGAGCAAGCGCTCAAGTATCAAGTATCAAGTATCAAGTATCAAGTATCAAGTAT 2517  
 Db 2462 GAGCGGAGAGCAAGCGCTCAAGTATCAAGTATCAAGTATCAAGTATCAAGTATCAAGTAT 2521  
 QY 2518 CTCGCGGAGCAGCATCTTTTGGGGGAACTCTCGGAAGGAGTCTTTTCAAGGCGCAGAAA 2577  
 Db 2522 CTCGCTTCTGACACTTTTGGGGGAACTCTCGGAAGGAGTCTTTTCAAGGCGCAGAAA 2581  
 QY 2578 AGGGTTCTCGAACTTTTGGGCTGTTTGAAGAGGTTGTTAAGAGCGGCGCTTACCGGAAAG 2637  
 Db 2582 AGGATTTCTGAACTTTTGGGCTGTTTGAAGAGGTTGTTAAGAGCGGCGCTTACCGGAAAG 2641  
 QY 2638 CGGA---TAGACGACCACTTTTCAAGAGAGAGGCTTCAAGAGCGGCTTACCGGAAAG 2693  
 Db 2642 AAGAGGCTCTAGAGAGAGTCTTCAAGAGAGAGTCTTCAAGAGCGGCTTACCGGAAAG 2701  
 QY 2694 GCCTTCCACTCTGACAGCGGAGTCTGAGAGGAGTCTGAGAGGAGTCTGAGAGGAGTCTGAG 2751  
 Db 2702 GGAACAGAGCTCTGAGAGAGAGTCTGAGAGGAGTCTGAGAGGAGTCTGAGAGGAGTCTGAG 2761

QY 2752 CCAGCCCAACAGCCTCAAGTTTGGAGCT-----GATACAAATGTTCTGCGGA 2799  
 Db 2762 CTTCCCCAGAGAGCACTTTTCCGAGCTATGTCTACTAGACTGAATGGTGGCAGCA 2821  
 QY 2800 GGTGGCGGCGCCATTGGCGCAAAATAACCAAGGTGCGATGGAGTGGCAATGCTTCGGGA 2859  
 Db 2822 GCTGGCGGAATGGTGGCGATGGCGGCAAAAGTGGCGAGGAGTGGTGAATGCTTCGGT 2881  
 QY 2860 GATTTGGATTTGGATTTCAAGTGGATGGGGGACAGAGTCTGTCACCAAGTCTCAACCGAAC 2919  
 Db 2882 GATTTGGATTTGGATTTCAAGTGGATGGGGGACAGAGTCTGTCACCAAGTCTCAACCGAAC 2941  
 QY 2920 TGGGTGCTGCGCAGCTCAACCAACCAAGTGGATGGGGGACAGAGTCTGTCACCAAGTCTCA 2979  
 Db 2942 TGGGTGCTGCGCAGCTCAACCAACCAAGTGGATGGGGGACAGAGTCTGTCACCAAGTCTCA 3001  
 QY 2980 GGAAGCAACGCGCAACGCTTCTTGGATACAGCACCCCTTGGGGTACTTTGACTTTTAAAC 3039  
 Db 3002 G-----ACACCTTCAACGGAATTTCTCCACCCCTGGGATATCTTTGACTTTTAAAC 3049  
 QY 3040 CGCTTCCACAGCAGCTGAGAGCCCGGAGACTGGGAAAGACTCATCAACAACTTACTTGGGCG 3099  
 Db 3050 CGCTTCCACAGCAGCTGAGAGCCCGGAGACTGGGAAAGACTCATCAACAACTTACTTGGGCG 3109  
 QY 3100 TTCAGACCCCGCTCCCTCAGAGTCAAAATCTTCAACATTTCAAGTCAAGAGAGTCAAGGTG 3159  
 Db 3110 CTGCGCCCAAAAGCATGCAAGTCCGATCTTCAACATTTCAAGTCAAGAGAGTCAAGGTG 3169  
 QY 3160 CAGGACTTCAACCAACCACTCGCCCAACCACTCACTCCACCTCCACCTTCAAGTCTTTCAGGAC 3219  
 Db 3170 TCTAAACGGGAGAGCAGCGTATCAACCACTCAACAGCAGCTTTCAGGAGTCTTTCAGGAG 3229  
 QY 3220 GACGACTACAGCTGCGCTCAGTCTGCGCAACCGGAGAGGAGTCTTTCAGGAGTCTTTCAGG 3279  
 Db 3230 AGCAGTACAGCTGCGCTCAGTCTGCGCAACCGGAGAGGAGTCTTTCAGGAGTCTTTCAGG 3289  
 QY 3280 CCTCGCAGGTTTTCAGCTGCGCAGTACGTTA---CGGAGCGCTGAACCGGAGAC 3336  
 Db 3290 CCCAACGAGTTCATGTTGCTCAGTACGAGTCTGCGGAGTCTGCGGAGTCTGCGGAGGAGC 3349  
 QY 3337 ACAGAAATCCCAACGAGAGGAGCAGCTTCTTCTGCTAGAGTACTTTCAGGAGAGTCTTTCAGG 3396  
 Db 3350 TCTCAAAACAGAGAGAGAGTCTTCTTCTGCTGAGTACTTTCAGGAGTCTTTCAGGAGAGT 3409  
 QY 3397 CTGAGAGCGGCAACAACTTTGATTTTCACTAAGTCTTTCAGGAGTCTTTCAGGAGTCTTTCAG 3456  
 Db 3410 CTGAGAGCGGCAACAACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3469  
 QY 3457 AGCTTCTGCTCCAGTCAAGACCTTTCAAGTGGCAACCGGCTGTTGGAGAGTCTTTCAGGAGT 3516  
 Db 3470 ATGTAAGTCAAGCAGAGCCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 3529  
 QY 3517 TACCGCTTCTGAGCAGCAAT-----AACACTGCGGAGTCTTTCAGGAGTCTTTCAGGAGAGT 3568  
 Db 3530 TGGGAGTCTCAGTCTACCACTCTGAGGAGTCTTCAACAGGAGTCTTTCAGGAGTCTTTCAGG 3589  
 QY 3569 TGGCGGAGATACGCGCAACA-----CTTCAAAAACCTTTCAGGAGTCTTTCAGGAGTCTTTCAG 3615  
 Db 3590 TTTTCCAAAGTCAACCAACCACTTTTCTGCTACCGCAAAACCTTTCAGGAGTCTTTCAGGAGT 3649  
 QY 3616 ATGGGCGGAGAGCAGGCTGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 3668  
 Db 3650 ATGATGAAGCAGAGAGTCTTCAAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 3709  
 QY 3669 CAGCGCTTCTGCGCAGCAACCAATAGGATGAGTCTGAGGAGGAGTCTTTCAGGAGTCTTTCAGG 3728  
 Db 3710 AGAAACCAAGTCTGCTTCTTATGAGCAGCAATCTTTCAGGAGTCTTTCAGGAGTCTTTCAGG 3769  
 QY 3729 GAGCGGAGAGGAGTCTGAGCAGCAACCTTTCAGGAGGAGTCTTTCAGGAGTCTTTCAGGAG 3788  
 Db 3770 TTTTGGC---CGGGAAACGGCATGCAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3828  
 QY 3789 TATGATCTTCAACAGCCAGCGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAGGAGTCTGAG 3848





```
QY 2912 CCCGAACCTGGGTGCTGCCAGCTACTAAACCAACCAAGTACCGAGAGATCAAAAGCGGCT 2971
Db 805 CCCGAACCTGGGTGCTGCCAGCTACTAAACCAACCAAGTACCGAGAGATCAAAAGCGGCT 864
QY 2972 CCGTCGAGGAGAGACAGCCCAACCGCTACTTTGGATGATGAGACCCCTCGGGGATCTTTG 3031
Db 865 CCGTCGAGGAGAGACAGCCCAACCGCTACTTTGGATGATGAGACCCCTCGGGGATCTTTG 924
QY 3032 ACTTTAAACCGCTTCCACAGCCACTGAGCCCGGAGCTGGCAAGAGCTCATCAACACT 3091
Db 925 ACTTTAAACCGCTTCCACAGCCACTGAGCCCGGAGCTGGCAAGAGCTCATCAACACT 984
QY 3092 ACTGGGGTTTCAGACCCCGGTCCTCAGAGTCAAAATCTTCAACATTCAAAGTCAAAAGG 3151
Db 985 ACTGGGGTTTCAGACCCCGGTCCTCAGAGTCAAAATCTTCAACATTCAAAGTCAAAAGG 1044
QY 3152 TCAGGTGACAGACTCCACACACAGCATCGGCAACACTCACTTCACCGTCCAAAGT 3211
Db 1045 TCAGGTGACAGACTCCACACACAGCATCGGCAACACTCACTTCACCGTCCAAAGT 1104
QY 3212 TTACGAGCAGCACTACCAAGTCCCTACGTCGCGCAAGTACGGTTACGCGACGCTGAACCGCG 3271
Db 1105 TTACGAGCAGCACTACCAAGTCCCTACGTCGCGCAAGTACGGTTACGCGACGCTGAACCGCG 1164
QY 3272 CGGCTTCCCTCCGAGGTCTTTACGTCGCGCAAGTACGGTTACGCGACGCTGAACCGCG 3331
Db 1165 CGGCTTCCCTCCGAGGTCTTTACGTCGCGCAAGTACGGTTACGCGACGCTGAACCGCG 1224
QY 3332 ACACACAGAAATCCACACAGAGGAGCAGCTTCTTCGCTAGAGTACTTTCCAGCA 3391
Db 1225 ACACACAGAAATCCACACAGAGGAGCAGCTTCTTCGCTAGAGTACTTTCCAGCA 1284
QY 3392 AGATGCTGAGAACGGGCAACAACTTTGAGTTTACCTACACTTTGAGGAGTGGCTTCC 3451
Db 1285 AGATGCTGAGAACGGGCAACAACTTTGAGTTTACCTACACTTTGAGGAGTGGCTTCC 1344
QY 3452 ACTCCAGCTTGGTCCAGTCAAGCACTGTTCAAGCTGGGCAACCCCGCTGGTGACCACT 3511
Db 1345 ACTCCAGCTTGGTCCAGTCAAGCACTGTTCAAGCTGGGCAACCCCGCTGGTGACCACT 1404
QY 3512 ACTGTACCGCTTGGTGAAGCAAAATTAACACTGGCGGAGTCCAGTTCAACAAAGAACCTGG 3571
Db 1405 ACTGTACCGCTTGGTGAAGCAAAATTAACACTGGCGGAGTCCAGTTCAACAAAGAACCTGG 1464
QY 3572 CCGGAGATACGCAACCACTTACAAACCTGTTCCCGGGGCCCATCGGCGGACCCAGG 3631
Db 1465 CCGGAGATACGCAACCACTTACAAACCTGTTCCCGGGGCCCATCGGCGGACCCAGG 1524
QY 3632 GCTGGAACCTGGGTCGGGGTCAACCGCGCCAGTGTACGGGCTTCGCCACGACCAATA 3691
Db 1525 GCTGGAACCTGGGTCGGGGTCAACCGCGCCAGTGTACGGGCTTCGCCACGACCAATA 1584
QY 3692 GGATGAGCTCGAGGGGCGAGTTACAGGTGCCCGCGAGCGCAACCGGATGACCAACA 3751
Db 1585 GGATGAGCTCGAGGGGCGAGTTACAGGTGCCCGCGAGCGCAACCGGATGACCAACA 1644
QY 3752 ACCTCAGGGGACCAACCACTATGCTGCGGAGCAACTATGATCTTCAACAGCGACCGG 3811
Db 1645 ACCTCAGGGGACCAACCACTATGCTGCGGAGCAACTATGATCTTCAACAGCGACCGG 1704
QY 3812 CGAACCCGGGCAACCGCGGACGTTACCTCGAGGGCAACATGCTCATCACCAGCGAGAGCG 3871
Db 1705 CGAACCCGGGCAACCGCGGACGTTACCTCGAGGGCAACATGCTCATCACCAGCGAGAGCG 1764
QY 3872 AGACGAGCCGGTGAACCGGCTGGGTTAAAGCTGGCGGCGAGTGGCCACCAACCAACC 3931
Db 1765 AGACGAGCCGGTGAACCGGCTGGGTTAAAGCTGGCGGCGAGTGGCCACCAACCAACC 1824
QY 3932 AGAGCTCCACACTGCCCCCGGACCGGACGCTACACCTCCAGGAAATGTCGCCGGCA 3991
Db 1825 AGAGCTCCACACTGCCCCCGGACCGGACGCTACACCTCCAGGAAATGTCGCCGGCA 1884
```

```
QY 3992 GCGTGTGATGAGAGGACGCTGTACTCTCAAGGAGCCCTCTGGGCCAAGATCCAGAGA 4051
Db 1895 GCGTGTGATGAGAGGACGCTGTACTCTCAAGGAGCCCTCTGGGCCAAGATCCAGAGA 1944
QY 4052 CGGGGGCGCACTTTTACCCCTCTCGGCGCATGGGCGGATTCGGAATCAAAACACCCACCGC 4111
Db 1945 CGGGGGCGCACTTTTACCCCTCTCGGCGCATGGGCGGATTCGGAATCAAAACACCCACCGC 2004
QY 4112 CCATGATGCTCATCAAGAACACGCGCTGTGCCCGGAAATATCACCAGCTTCTCGGACGTGC 4171
Db 2005 CCATGATGCTCATCAAGAACACGCGCTGTGCCCGGAAATATCACCAGCTTCTCGGACGTGC 2064
QY 4172 CCGTCAGCAGCTTCATCAACCCAGTACAGCACCGGCGAGTCCACGTCGAGATGAGTGGG 4231
Db 2065 CCGTCAGCAGCTTCATCAACCCAGTACAGCACCGGCGAGTCCACGTCGAGATGAGTGGG 2124
QY 4232 AGCTCAAGAGGAGAAATCTCAAGAGGTGGAAACCCAGAGATCCAGTACACAAACAACTACA 4291
Db 2125 AGCTCAAGAGGAGAAATCTCAAGAGGTGGAAACCCAGAGATCCAGTACACAAACAACTACA 2184
QY 4292 ACACACCCCGCTTTGTGGACTTTGCCCGGACAGCACCGGGAATACAGAACCCACGAC 4351
Db 2185 ACACACCCCGCTTTGTGGACTTTGCCCGGACAGCACCGGGAATACAGAACCCACGAC 2244
QY 4352 CTATCGGAACCCGATACCTTACCCGACCCCTTTAACCCATTCATGTCGCATACCTCAAT 4411
Db 2245 CTATCGGAACCCGATACCTTACCCGACCCCTTTAACCCATTCATGTCGCATACCTCAAT 2304
QY 4412 AAA 4414
Db 2305 AAA 2307

RESULT 7
AX256327
LOCUS AX256327 2307 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 7 from Patent WO0170276.
ACCESSION AX256327
VERSION AX256327.1 GI:16075184
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chiorini, J.A., Kotin, R.M., Davidson, B. and Zabner, J.
TITLE AAV5 vector for transducing brain cells and lung cells
JOURNAL Patent: WO 0170276-A 7 27-SEP-2001;
The Secretary, Department of Health and Human Services (US);
University of Iowa Research Foundation (US);
FEATURES
source
1..2307
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Note = synthetic construct"

ORIGIN

Query Match 47.8%; Score 2223; DB 6; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2192 AGTAATAAGCGAGTAGTCATGCTCTTTGTTGATCACCCTCCAGATTGTTGGAAGAAG 2251
Db 85 AGTAATAAGCGAGTAGTCATGCTCTTTGTTGATCACCCTCCAGATTGTTGGAAGAAG 144
QY 2252 TTGGTGAAGGTCTTCGCGAGTTTTCGGGCTTGAAGCGGCGCCACCGAAACCAACCCCA 2311
Db 145 TTGGTGAAGGTCTTCGCGAGTTTTCGGGCTTGAAGCGGCGCCACCGAAACCAACCCCA 204
QY 2312 ATCAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCTGGTTATACTATCTCGGAC 2371
Db 205 ATCAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCTGGTTATACTATCTCGGAC 264
```

QY 2372 CCGGAAACGGTCTCGATCAGGAGAGCCTGTCAAACAGGCGACAGAGGTGCGCGAGAGC 2431  
 Db |||||  
 QY 265 CCGGAAACGGTCTCGATCAGGAGAGCCTGTCAAACAGGCGACAGAGGTGCGCGAGAGC 324  
 Db |||||  
 QY 2432 ACACATCTCTGTAACAGAGAGCTTTGAGCGCGGAGACAAACCCCTACCTCAAGTCAACC 2491  
 Db |||||  
 QY 325 ACACATCTCTGTAACAGAGAGCTTTGAGCGCGGAGACAAACCCCTACCTCAAGTCAACC 384  
 Db |||||  
 QY 2492 AGCGGAGCGCGAGCTTTGAGGAGAGCTGCGGACGACATCTTTCGGGGGAAACCTCG 2551  
 Db |||||  
 QY 385 AGCGGAGCGCGAGCTTTGAGGAGAGCTGCGGACGACATCTTTCGGGGGAAACCTCG 444  
 Db |||||  
 QY 2552 GAAAGGAGCTTTGAGGAGAGCTTTGAGGAGAGCTTTGAGGAGAGCTTTGAGGAGAG 2611  
 Db |||||  
 QY 445 GAAAGGAGCTTTGAGGAGAGCTTTGAGGAGAGCTTTGAGGAGAGCTTTGAGGAGAG 504  
 Db |||||  
 QY 2612 GTGCTAAGAGCGGCCCTACCGGAAAGCGGATAGACGACCTTTTCAAAAAGAAAGAGG 2671  
 Db |||||  
 QY 505 GTGCTAAGAGCGGCCCTACCGGAAAGCGGATAGACGACCTTTTCAAAAAGAAAGAGG 564  
 Db |||||  
 QY 2672 CTCGGACGAAAGAGCTTCCAGGCTTCCAGCTTCCAGGCGGAGCTGGACCCAGCG 2731  
 Db |||||  
 QY 565 CTCGGACGAAAGAGCTTCCAGGCTTCCAGCTTCCAGGCGGAGCTGGACCCAGCG 624  
 Db |||||  
 QY 2732 GATCCAGAGCTGCAAAATCCAGGCCAACCGACCTCAAGTTTGGAGCTGATACAAATG 2791  
 Db |||||  
 QY 625 GATCCAGAGCTGCAAAATCCAGGCCAACCGACCTCAAGTTTGGAGCTGATACAAATG 684  
 Db |||||  
 QY 2792 CTCGGGAGGTGGCGCCCATTTGGGCGCAAAATAACAGGTGCGATGAGTGGGCAATG 2851  
 Db |||||  
 QY 685 CTCGGGAGGTGGCGCCCATTTGGGCGCAAAATAACAGGTGCGATGAGTGGGCAATG 744  
 Db |||||  
 QY 2852 CTCGGGAGATGGCAATTTGGGCTTCCAGTGGATGGGCGACAGCTGTCACCAAGTCCA 2911  
 Db |||||  
 QY 745 CTCGGGAGATGGCAATTTGGGCTTCCAGTGGATGGGCGACAGCTGTCACCAAGTCCA 804  
 Db |||||  
 QY 2912 CCGGAACCTGGGTGCTGCCAGCTACAAACCAACAGTACCGAGAGATCAAAAGCGGT 2971  
 Db |||||  
 QY 805 CCGGAACCTGGGTGCTGCCAGCTACAAACCAACAGTACCGAGAGATCAAAAGCGGT 864  
 Db |||||  
 QY 2972 CGGTGACGGAAGCAACGCGCAACGCTTCTTTGGATACAGCAACCCCTGGGGGTACTTTG 3031  
 Db |||||  
 QY 865 CGGTGACGGAAGCAACGCGCAACGCTTCTTTGGATACAGCAACCCCTGGGGGTACTTTG 924  
 Db |||||  
 QY 3032 ACTTTAAACGCTTCCAGAGCACTGGAGCCCGAGAGCTGGCAAGAGCTCATCAACAAT 3091  
 Db |||||  
 QY 925 ACTTTAAACGCTTCCAGAGCACTGGAGCCCGAGAGCTGGCAAGAGCTCATCAACAAT 984  
 Db |||||  
 QY 3092 ACTGGGCTTTCAGACCCCGGTCCCTCAGAGTCAAAATCTTCAACATTTCAAGTCAAAAGAGG 3151  
 Db |||||  
 QY 985 ACTGGGCTTTCAGACCCCGGTCCCTCAGAGTCAAAATCTTCAACATTTCAAGTCAAAAGAGG 1044  
 Db |||||  
 QY 3152 TCAAGGTGAGAGCTTCCACCAACCAATCGCAGCAACCACTCACTCCACCTGCAAGTGT 3211  
 Db |||||  
 QY 1045 TCACGCTGAGAGCTTCCACCAACCAATCGCAGCAACCACTCACTCCACCTGCAAGTGT 1104  
 Db |||||  
 QY 3212 TTACGAGACGAGCTTACAGCTGCTTACGCTGCTGCGCAACGAGGATGCTGCTG 3271  
 Db |||||  
 QY 1105 TTACGAGACGAGCTTACAGCTGCTTACGCTGCTGCGCAACGAGGATGCTGCTG 1164  
 Db |||||  
 QY 3272 CGGCTTTCCCTCCGAGGCTTTTACGCTGCGGAGTACGCTTACGAGAGCTGAAACCGCG 3331  
 Db |||||  
 QY 1165 CGGCTTTCCCTCCGAGGCTTTTACGCTGCGGAGTACGCTTACGAGAGCTGAAACCGCG 1224  
 Db |||||  
 QY 3332 ACAACAGAAATCCACGAGAGGAGCTTCTTCTGCTAGAGTACTTTCCAGCA 3391  
 Db |||||  
 QY 1225 ACAACAGAAATCCACGAGAGGAGCTTCTTCTGCTAGAGTACTTTCCAGCA 1284  
 Db |||||  
 QY 3392 AGATGCTGAGACGGGCAACATTTGAGTGTACTTCAACATTTGAGGAGGTGCTTCC 3451  
 Db |||||  
 QY 1285 AGATGCTGAGACGGGCAACATTTGAGTGTACTTCAACATTTGAGGAGGTGCTTCC 1344  
 Db |||||  
 QY 3452 ACTCCAGCTTCGCTCCAGTCCAGAACCTGTTCAAGTGGGCAACCCCGTGTGAGACAGT 3511  
 Db |||||

Db |||||  
 QY 1345 ACTCCAGCTTCGCTCCAGTCCAGAACCTGTTCAGAGTGGCCAAACCCGTGTGGACCACT 1404  
 QY 3512 ACTTGTACCGCTTCGTGAGCAAAATAACACTGGCGGAGTCCAGTTCACCAAGAACCTGG 3571  
 Db 1405 ACTTGTACCGCTTCGTGAGCAAAATAACACTGGCGGAGTCCAGTTCACCAAGAACCTGG 1464  
 QY 3572 CCGGAGATAGCGCCAAACACCTACAAAACTGTGTTCCCGGGGCCCATGCGGCCGAAACCGAG 3631  
 Db 1465 CCGGAGATAGCGCCAAACACCTACAAAACTGTGTTCCCGGGGCCCATGCGGCCGAAACCGAG 1524  
 QY 3632 GGTGAAACCTGGGCTTCGGGCTCAACCGGCGAGTGTGAGCGCTTTCGCGACGACCAATA 3691  
 Db 1525 GGTGAAACCTGGGCTTCGGGCTCAACCGGCGAGTGTGAGCGCTTTCGCGACGACCAATA 1584  
 QY 3692 GGATCGAGCTCGAGGCGCGAGTGTACCAAGTGTCCCGCGAGCGCAACGCGCATGACCAACA 3751  
 Db 1585 GGATCGAGCTCGAGGCGCGAGTGTACCAAGTGTCCCGCGAGCGCAACGCGCATGACCAACA 1644  
 QY 3752 ACCTCCAGGCGCAGCAACACCTATGCTTGGAGAAACACTATGATCTTCAACAGCGACCGG 3811  
 Db 1645 ACCTCCAGGCGCAGCAACACCTATGCTTGGAGAAACACTATGATCTTCAACAGCGACCGG 1704  
 QY 3812 CGAAACCGGCGACCGCGCGACCTGACCTGAGGCGAAACATGCTCATCACAGCGAGCG 3871  
 Db 1705 CGAAACCGGCGACCGCGCGACCTGACCTGAGGCGAAACATGCTCATCACAGCGAGCG 1764  
 QY 3872 AGACGCGAGCGGTGAACCGCGTGGGCTGTAACAAGTGTGCGCGGAGATGGCCACCAACC 3931  
 Db 1765 AGACGCGAGCGGTGAACCGCGTGGGCTGTAACAAGTGTGCGCGGAGATGGCCACCAACC 1824  
 QY 3932 AGAGCTTCCACCTGCTCCCGCGACCGCAACGTAACCTCCAGGAAATCTGTCGCCGCA 3991  
 Db 1825 AGAGCTTCCACCTGCTCCCGCGACCGCAACGTAACCTCCAGGAAATCTGTCGCCGCA 1884  
 QY 3992 GCGTGTGATGAGAGGAGCGGTGTACCTCCAGGACCCATCTGGGCGAAGATCCAGAGA 4051  
 Db 1885 GCGTGTGATGAGAGGAGCGGTGTACCTCCAGGACCCATCTGGGCGAAGATCCAGAGA 1944  
 QY 4052 CGGGGCGCACTTTCAACCCCTCTCCGGCCATGGGCGGATTCGAGCTCAAAACCCACCGC 4111  
 Db 1945 CGGGGCGCACTTTCAACCCCTCTCCGGCCATGGGCGGATTCGAGCTCAAAACCCACCGC 2004  
 QY 4112 CCATGATGCTCATCAAGAACACGCTGTGCGCGGAAATATCACAGTTCGCGAGTGC 4171  
 Db 2005 CCATGATGCTCATCAAGAACACGCTGTGCGCGGAAATATCACAGTTCGCGAGTGC 2064  
 QY 4172 CGGTGAGAGCTTCATCACCCAGTACAGCACCGGCGAGTTCACCGTGGAGTGGAGTGGG 4231  
 Db 2065 CGGTGAGAGCTTCATCACCCAGTACAGCACCGGCGAGTTCACCGTGGAGTGGAGTGGG 2124  
 QY 4232 AGCTCAAGAGGAAACCTCCAAGAGTGGAAACCCAGAGATCCAGTACACAAACACTACA 4291  
 Db 2125 AGCTCAAGAGGAAACCTCCAAGAGTGGAAACCCAGAGATCCAGTACACAAACACTACA 2184  
 QY 4292 ACACCCCGAGTGTGGAGCTTTGCGCGGAGACGACCGCGGAAATACAGAACCCAGAC 4351  
 Db 2185 ACACCCCGAGTGTGGAGCTTTGCGCGGAGACGACCGCGGAAATACAGAACCCAGAC 2244  
 QY 4352 CTATCGGACCCGATACCTTACCCGACCCCTTTAAACCCATTCATGTGCGATACCTCAAT 4411  
 Db 2245 CTATCGGACCCGATACCTTACCCGACCCCTTTAAACCCATTCATGTGCGATACCTCAAT 2304  
 QY 4412 AAA 4414  
 Db 2305 AAA 2307

RESULT 8  
 BD211183  
 LOCUS  
 DEFINITION AAV5 vector and uses thereof.  
 ACCESSION BD211183

linear PAT 17-JUL-2003

2264 bp

BD211183

VERSION	BD211183.1	GI:33020953	
KEYWORDS	JP 2002516092-A/3		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 2264)		
AUTHORS	Chlorini, J.A. and Kotin, R.M.		
TITLE	AAV5 vector and uses thereof		
JOURNAL	Patent: JP 2002516092-A 3 04-JUN-2002;		
COMMENT	THE UNITED STATES OF AMERICA		
	OS Artificial Sequence		
	PN JP 2002516092-A/3		
	PD 04-JUN-2002		
	PF 28-MAY-1999 JP 2000550986		
	PR 28-MAY-1998 US 60/087029		
	PI JOHN A CHIORINI, ROBERT M KOTIN		
	PC C12N15/09, C07K14/015, C07K16/08, C12N7/00, C12Q1/68, G01N33/15, PC		
	G01N33/50,		
	PC C12N15/00		
	CC Description of Artificial Sequence; Note = synthetic construct		
	FH Key	Location/Qualifiers	
	FT source	1..2264	
FEATURES	Location/Qualifiers	/organism='Artificial Sequence'.	
source	1..2264		
ORIGIN	/organism="synthetic construct"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
Query Match	46.9%; Score 2181.4; DB 6; Length 2264;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2182; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY 2232	TCCAGATTGTTGGAAGAGTGTGTTGAGTCTTCGGAGTTCCTGGAGTTTGGCCCTTGAAGCGG	2291	
DB 82	TCAAGATTGTTGGAAGAGTGTGTTGAGTCTTCGGAGTTCCTGGAGTTTGGCCCTTGAAGCGG	141	
QY 2292	CCACCGAAACCAAAACCAATCAGCAGCATCAAGATCAAGCCCGTGTCTTGTGCTGCC	2351	
DB 142	CCACCGAAACCAAAACCAATCAGCAGCATCAAGATCAAGCCCGTGTCTTGTGCTGCC	201	
QY 2352	TGTTATTAATCTATCTCGGACCGGAAACCGGTCTCGATCGAGGAGAGCTGTCAACAGGGC	2411	
DB 202	TGTTATTAATCTATCTCGGACCGGAAACCGGTCTCGATCGAGGAGAGCTGTCAACAGGGC	261	
QY 2412	AGACGAGTCTCGGAGAGCAGCAGCATCTCGTACAAAGAGAGTTCGATCGAGGAGAGCTGTCAACAGGGC	2471	
DB 262	AGACGAGTCTCGGAGAGCAGCAGCATCTCGTACAAAGAGAGTTCGATCGAGGAGAGCTGTCAACAGGGC	321	
QY 2472	CCCTTACCTCAAGTACAAACCAACCGGACCGGAGTTCAGGAGAGCTCGCCGACGAC	2531	
DB 322	CCCTTACCTCAAGTACAAACCAACCGGACCGGAGTTCAGGAGAGCTCGCCGACGAC	381	
QY 2532	ATCCTTCGGGGAAACCTCGGAAAGCAGTCTTTTCAGGCCCAAGAAAGGTTCTCGAAC	2591	
DB 382	ATCCTTCGGGGAAACCTCGGAAAGCAGTCTTTTCAGGCCCAAGAAAGGTTCTCGAAC	441	
QY 2592	TTTTCGGCTGTTGAGAGGAGTCTAGACGGCCCTTACCGGAAAGCGGATAGACGACCA	2651	
DB 442	TTTTCGGCTGTTGAGAGGAGTCTAGACGGCCCTTACCGGAAAGCGGATAGACGACCA	501	
QY 2652	CTTTTCCAAAAGAAAGAGTCTCGGACCGGAGAGTCTCAAGCTTCCACCTTCGTGAGA	2711	
DB 502	CTTTTCCAAAAGAAAGAGTCTCGGACCGGAGAGTCTCAAGCTTCCACCTTCGTGAGA	561	
QY 2712	CGCGAAGCTGGACCGAGCGGATCCAGAGTGTCAAAATCCAGCCCAACAGCCTCAAG	2771	
DB 562	CGCGAAGCTGGACCGAGCGGATCCAGAGTGTCAAAATCCAGCCCAACAGCCTCAAG	621	
QY 2772	TTTTCGGAGCTGATACATGTTCTGGGAGTGTGGGCGGCTTGGGCGACAAATTAACAAAG	2831	
DB 622	TTTTCGGAGCTGATACATGTTCTGGGAGTGTGGGCGGCTTGGGCGACAAATTAACAAAG	681	
QY 2832	TGCGATGAGTGGCAATGCTCGGGAGATTGCAATTGCGATTTCACGTGATGGGGA	2891	
DB 682	TGCGATGAGTGGCAATGCTCGGGAGATTGCAATTGCGATTTCACGTGATGGGGA	741	
QY 2892	CAGAGTCTGTCACCAAGTCCACCCGAACTGGTGTGCTGCCAGCTACAAACACCAACAGTA	2951	
DB 742	CAGAGTCTGTCACCAAGTCCACCCGAACTGGTGTGCTGCCAGCTACAAACACCAACAGTA	801	
QY 2952	CGGAGATCAAAAAGCGGCTCGTTCGAGGAGCAACGCCAAGCGCTACTTTGGATACAG	3011	
DB 802	CGGAGATCAAAAAGCGGCTCGTTCGAGGAGCAACGCCAAGCGCTACTTTGGATACAG	861	
QY 3012	CACCCCTCGGGGTACTTTGACTTAAACCGTTCACAGCAGTTCGAGGAGGAGGAGTGTG	3071	
DB 862	CACCCCTCGGGGTACTTTGACTTAAACCGTTCACAGCAGTTCGAGGAGGAGGAGTGTG	921	
QY 3072	GCAAGAGTCTCAACAACTACTGGGCTTCAGAGCCCGGCTCCCTCAGAGTCAAAATCTT	3131	
DB 922	GCAAGAGTCTCAACAACTACTGGGCTTCAGAGCCCGGCTCCCTCAGAGTCAAAATCTT	981	
QY 3132	CAACATTCAGTCAAAAAGGTCACGGTTCAGAGTTCACCAACCAACCAACCAACCT	3191	
DB 982	CAACATTCAGTCAAAAAGGTCACGGTTCAGAGTTCACCAACCAACCAACCAACCT	1041	
QY 3192	CACCTCCACCGTCCAAAGTGTTCAGGAGGAGTTCACAGTCCCTCAGTGTGCGGAA	3251	
DB 1042	CACCTCCACCGTCCAAAGTGTTCAGGAGGAGTTCACAGTCCCTCAGTGTGCGGAA	1101	
QY 3252	CGGACCGAGGATGCTTCGGGCTTCCTTCGGAGTCTTTACGTCGCGAGTACGG	3311	
DB 1102	CGGACCGAGGATGCTTCGGGCTTCCTTCGGAGTCTTTACGTCGCGAGTACGG	1161	
QY 3312	TTACGCAAGTCAAAACCGGACCAACAGAAATCCACCGAGAGGAGTCTTCTCTG	3371	
DB 1162	TTACGCAAGTCAAAACCGGACCAACAGAAATCCACCGAGAGGAGTCTTCTCTG	1221	
QY 3372	CCTAGAGTACTTCCAGCAGAGTGTGAGAACCGGCAACAACTTTGAGTTTACCTACAA	3431	
DB 1222	CCTAGAGTACTTCCAGCAGAGTGTGAGAACCGGCAACAACTTTGAGTTTACCTACAA	1281	
QY 3432	CTTTGAGAGTGTGCTTCCTTCAGTTCCTTCAGTTCCTTCAGTTCCTTCAGTTCCT	3491	
DB 1282	CTTTGAGAGTGTGCTTCCTTCAGTTCCTTCAGTTCCTTCAGTTCCTTCAGTTCCT	1341	
QY 3492	CAACCCCTCGTGGACAGTACTTGTACCGCTTCGTGAGCACAATAACACTTGGCGAGT	3551	
DB 1342	CAACCCCTCGTGGACAGTACTTGTACCGCTTCGTGAGCACAATAACACTTGGCGAGT	1401	
QY 3552	CCAGTTCAACAAAGAACTTCGCGGAGATAGCGCAACCTCAAAACTTGGTTCCCGGG	3611	
DB 1402	CCAGTTCAACAAAGAACTTCGCGGAGATAGCGCAACCTCAAAACTTGGTTCCCGGG	1461	
QY 3612	GCCCATGGGCGGAAACCCAGGCTGGAACCTCGGCTTCGGGCTCAACCGCCAGTGTGAG	3671	
DB 1462	GCCCATGGGCGGAAACCCAGGCTGGAACCTCGGCTTCGGGCTCAACCGCCAGTGTGAG	1521	
QY 3672	CGCTTCGCGCACCAATAGGATGAGTTCGAGGCGCGAGTTACCGAGTGTGCGGCGCA	3731	
DB 1522	CGCTTCGCGCACCAATAGGATGAGTTCGAGGCGCGAGTTACCGAGTGTGCGGCGCA	1581	
QY 3732	GCCGAAAGGATGACCAACCTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTC	3791	
DB 1582	GCCGAAAGGATGACCAACCTTCAGGAGGAGTTCAGGAGGAGTTCAGGAGGAGTTC	1641	
QY 3792	GATCTTCAACAGCGAGCGGAAACCCGGGCAACCGCCAGTTCCTCGAGGAGTTC	3851	
DB 1642	GATCTTCAACAGCGAGCGGAAACCCGGGCAACCGCCAGTTCCTCGAGGAGTTC	1701	
QY 3852	GCTCATCACCGAGGAGGAGCGAGCGCGGTGAAACCGCGTGGCGTACAACTCGCGCG	3911	
DB 1702	GCTCATCACCGAGGAGGAGCGAGCGCGGTGAAACCGCGTGGCGTACAACTCGCGCG	1761	

3912 GCAGATGGCCACCAACACAGAGCTCCACACTGCCCCCGGACCGGCACGTACAACT 3971  
Db GAGATGGCCACCAACACAGAGCTCCACACTGCCCCCGGACCGGCACGTACAACT 1821  
3972 CAGGAAATCGTCCCGGAGCGTGTGGATGGAGAGGACGTGTACTCCAGGACCCAT 4031  
Db CCAGGAAATCGTCCCGGAGCGTGTGGATGGAGAGGACGTGTACTCCAGGACCCAT 1881  
4032 CTGGGCAAGATCCCAAGACCGGGCGCACTTTCACCCCTCTCCGGCCATGGCGGATT 4091  
Db CTGGGCAAGATCCCAAGACCGGGCGCACTTTCACCCCTCTCCGGCCATGGCGGATT 1941  
4092 CGGACTCAAAACACCCACCGCCATGCTCATCAAGAACACGCTGTGCCGGAAATAT 4151  
Db CGGACTCAAAACACCCACCGCCATGCTCATCAAGAACACGCTGTGCCGGAAATAT 2001  
4152 CACCACTTCTCGGAGTGGCCGTCAGAGCTTCATCACCAGTACAGCACCGGAGGT 4211  
Db CACCACTTCTCGGAGTGGCCGTCAGAGCTTCATCACCAGTACAGCACCGGAGGT 2061  
4212 CACCGTGGAGTGGAGTGGAGCTCAAGAGGAAACTCCAGAGGTGGAACCCAGAGAT 4271  
Db CACCGTGGAGTGGAGTGGAGCTCAAGAGGAAACTCCAGAGGTGGAACCCAGAGAT 2121  
4272 CCAGTACAAACAACTACAACACCCCACTTTGTGACTTTGCCCGGACAGCACCGG 4331  
Db CCAGTACAAACAACTACAACACCCCACTTTGTGACTTTGCCCGGACAGCACCGG 2181  
4332 GGAATCAGAACACACGACTTACGAAACCCGATACCTTACCGGACCCCTTAAACCCAT 4391  
Db GGAATCAGAACACACGACTTACGAAACCCGATACCTTACCGGACCCCTTAAACCCAT 2241  
4392 TCATGTGCGATACCTCAATAAA 4414  
Db TCATGTGCGATACCTCAATAAA 2264

RESULT 9  
BD211184  
LOCUS BD211184 2264 bp DNA linear PAT 17-JUL-2003  
DEFINITION AAV5 vector and uses thereof.  
ACCESSION BD211184  
VERSION BD211184.1 GI:33020954  
KEYWORDS JP 2002516092-A/4.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 2264)  
AUTHORS Chiorini, J.A. and Kotin, R.M.  
TITLE AAV5 vector and uses thereof  
JOURNAL Patent: JP 2002516092-A 4 04-JUN-2002;  
THE UNITED STATES OF AMERICA  
COMMENT OS Artificial Sequence  
PN JP 2002516092-A/4  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000550986  
PR 28-MAY-1998 US 60/087029  
PI JOHN A. CHIORINI, ROBERT M. KOTIN  
PC C12N15/09, C07K14/015, C07K16/08, C12N7/00, C12Q1/68, G01N33/15, PC  
G01N33/50,  
PC C12N15/00  
CC Description of Artificial Sequence:/Note = synthetic construct  
FH Key Location/Qualifiers  
FT source 1..2264  
FT /organism='Artificial Sequence'.  
FEATURES  
source  
1..2264  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 46.9%; Score 2181.4; DB 6; Length 2264;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2232 TCCAGATGGTTGGAGAGTTGGTGAAGGTCTTCGCGAGTTTGGGCTTTGAAGCGG 2291  
Db 82 TCAAGATGGTTGGAGAGTTGGTGAAGGTCTTCGCGAGTTTGGGCTTTGAAGCGG 141  
QY 2292 CCCACGAAACCAAAACCAATCAGAGCATCAAGTCAAGCCCGTGTCTGTGCTGCC 2351  
Db 142 CCCACGAAACCAAAACCAATCAGAGCATCAAGTCAAGCCCGTGTCTGTGCTGCC 201  
QY 2352 TGGTTATAACTCTCGGACCCGAAACCGTCTCGATCGAGAGAGCTGTCAACAGGGC 2411  
Db 202 TGGTTATAACTCTCGGACCCGAAACCGTCTCGATCGAGAGAGCTGTCAACAGGGC 261  
QY 2412 AGACGAGGTGCGCGAGAGCAGCATCTCTGATCAACAGAGAGCTTTGAGCGGGAGACAA 2471  
Db 262 AGACGAGGTGCGCGAGAGCAGCATCTCTGATCAACAGAGAGCTTTGAGCGGGAGACAA 321  
QY 2472 CCCCTACCTCAAGTCAACACCGGAGCGCGAGTTTCAAGAGAGCTCGCGAGAGCAC 2531  
Db 322 CCCCTACCTCAAGTCAACACCGGAGCGCGAGTTTCAAGAGAGCTCGCGAGAGCAC 381  
QY 2532 ATCCTTCGGGGGAAACCTCGGAAAGCGAGTCTTTAGGCCCAAGAAAGGTTCTCGAAC 2591  
Db 382 ATCCTTCGGGGGAAACCTCGGAAAGCGAGTCTTTAGGCCCAAGAAAGGTTCTCGAAC 441  
QY 2592 TTTTGGCCCTGGTTGAAGAGGGTGTAAAGACGGGCCCTACCGGAAAGCGGATAGACCA 2651  
Db 442 TTTTGGCCCTGGTTGAAGAGGGTGTAAAGACGGGCCCTACCGGAAAGCGGATAGACCA 501  
QY 2652 TTTTCAAAGAAAGAGAGGCTCGGACCGAGAGGACTTCAAGCCTTCCACCTCGTCAGA 2711  
Db 502 TTTTCAAAGAAAGAGAGGCTCGGACCGAGAGGACTTCAAGCCTTCCACCTCGTCAGA 561  
QY 2712 CGCGAGGTGAGCCAGCGGATCCAGAGCTGCAAAATCCAGAGCCCAACAGCCTCAAG 2771  
Db 562 CGCGAGGTGAGCCAGCGGATCCAGAGCTGCAAAATCCAGAGCCCAACAGCCTCAAG 621  
QY 2772 TTTTGGAGGTGATACAAATGTCTCGGAGGTGCGGCCCATTTGGGGACAAATACCAAG 2831  
Db 622 TTTTGGAGGTGATACAAATGTCTCGGAGGTGCGGCCCATTTGGGGACAAATACCAAG 681  
QY 2832 TGCCGATGGAGTGGGCAATGCTTCGCGAGATTGGCATTTCCAGCTTGGATGGGGA 2891  
Db 682 TGCCGATGGAGTGGGCAATGCTTCGCGAGATTGGCATTTCCAGCTTGGATGGGGA 741  
QY 2892 CAGAGTGTCAACCAAGTCCACCGGACCTCGGCTGCTCCAGAGCTTACCAACCAAGT 2951  
Db 742 CAGAGTGTCAACCAAGTCCACCGGACCTCGGCTGCTCCAGAGCTTACCAACCAAGT 801  
QY 2952 CCGAGAGATCAAAAGCGGCTCCGTTCGACGGAAGCAACGCAACGCTTCTTTGGATACG 3011  
Db 802 CCGAGAGATCAAAAGCGGCTCCGTTCGACGGAAGCAACGCAACGCTTCTTTGGATACG 861  
QY 3012 CACCCCTGGGGGTACTTTGATTTAACCGCTTCCAGAGCTTGGAGAGCCCGGAGCTG 3071  
Db 862 CACCCCTGGGGGTACTTTGATTTAACCGCTTCCAGAGCTTGGAGAGCCCGGAGCTG 921  
QY 3072 GCAAGACTCATCAACAACTACTGGGCTTTCAGAGCCCGGCTCCCTCAGAGTCAAAATCTT 3131  
Db 922 GCAAGACTCATCAACAACTACTGGGCTTTCAGAGCCCGGCTCCCTCAGAGTCAAAATCTT 981  
QY 3132 CAACATTCAAGTCAAGAGGTTCAGCGTGCAGGACTCCACCAACCAACCAACCAACCT 3191  
Db 982 CAACATTCAAGTCAAGAGGTTCAGCGTGCAGGACTCCACCAACCAACCAACCAACCT 1041  
QY 3192 CACCTCCAGCTCCAGTGTTCAGAGAGGACTTACAGTCCCTACGTCGTCGCA 3251  
Db 1042 CACCTCCAGCTCCAGTGTTCAGAGAGGACTTACAGTCCCTACGTCGTCGCA 1101  
QY 3252 CGGACCGAGGATGCTTCGCGGCTTCCCTCCAGAGTCTTTACGCTGCGGAGTACGG 3311

Db 1102 CGGACCGAGGATGCTCTGCCGGCTTCCCTCCGAGGTCTTTACGCTGCCGACGAGTACGG 1161  
Qy 3312 TTACGCGACGCTGAACCGCGACAAACACAGAAATCCCAACGAGAGGACGCTTCTTCTG 3371  
Db 1162 TTACGCGACGCTGAACCGCGACAAACACAGAAATCCCAACGAGAGGACGCTTCTTCTG 1221  
Qy 3372 CCTAGAGTACTTTCCAGCAAGATGCTGAGAACGGCAACAACTTTGAGTTTACCTACAA 3431  
Db 1222 CCTAGAGTACTTTCCAGCAAGATGCTGAGAACGGCAACAACTTTGAGTTTACCTACAA 1281  
Qy 3432 CTTTGGAGAGTGGCTTCCACTCCAGCTTCCCTCCAGTCCAGAACCTGTTCAAGCTGGC 3491  
Db 1282 CTTTGGAGAGTGGCTTCCACTCCAGCTTCCCTCCAGTCCAGAACCTGTTCAAGCTGGC 1341  
Qy 3492 CAACCCGCTGTGGACCACTACTTGTACCGCTTCTGTAGACAAATAACACTGGCGGAGT 3551  
Db 1342 CAACCCGCTGTGGACCACTACTTGTACCGCTTCTGTAGACAAATAACACTGGCGGAGT 1401  
Qy 3552 CCAGTTCAACAGAACTTGGCCGGGAGATACGCCAACACCTTACAAAACTGTTTCCCGGG 3611  
Db 1402 CCAGTTCAACAGAACTTGGCCGGGAGATACGCCAACACCTTACAAAACTGTTTCCCGGG 1461  
Qy 3612 GCCCATGGCCGAACCCAGGCTGGAACTGGCTCCGGGTCCAGCGGCTCAACCGGCGAGTGCAG 3671  
Db 1462 GCCCATGGCCGAACCCAGGCTGGAACTGGCTCCGGGTCCAGCGGCTCAACCGGCGAGTGCAG 1521  
Qy 3672 CGCCTTCCGCCACGACCAATAGATGGAGCTCGAGGGCGGAGTTACAGAGTGCCCGCGCA 3731  
Db 1522 CGCCTTCCGCCACGACCAATAGATGGAGCTCGAGGGCGGAGTTACAGAGTGCCCGCGCA 1581  
Qy 3732 GCCGAAACGCGATGACCAACACCTCCAGGGCAGCAACCTATGCTTCCCTGGAGAACACTAT 3791  
Db 1582 GCCGAAACGCGATGACCAACACCTCCAGGGCAGCAACCTATGCTTCCCTGGAGAACACTAT 1641  
Qy 3792 GATCTTCAACAGCAGCGCGGACACCGGACCAACCGCAGCTACCTCGAGGGCAACAT 3851  
Db 1642 GATCTTCAACAGCAGCGCGGACACCGGACCAACCGCAGCTACCTCGAGGGCAACAT 1701  
Qy 3852 GCTCATCACAGCAGCAGCAGCAGCGGCTGAAACCGGCTGGCTACACAGCTGCGCGG 3911  
Db 1702 GCTCATCACAGCAGCAGCAGCAGCGGCTGAAACCGGCTGGCTACACAGCTGCGCGG 1761  
Qy 3912 GCAGATGGCCACCAACCAACAGAGCTCCACCTGCCCGCCGACCGGACGTCACACCT 3971  
Db 1762 GCAGATGGCCACCAACCAACAGAGCTCCACCTGCCCGCCGACCGGACGTCACACCT 1821  
Qy 3972 CCAGGAATCGTCCCGGACGCTGAGTGGAGAGGAGCGTGTACCTCCAGAACCCAT 4031  
Db 1822 CCAGGAATCGTCCCGGACGCTGAGTGGAGAGGAGCGTGTACCTCCAGAACCCAT 1891  
Qy 4032 CTGGGCCAAGATCCAGAGACGGGGCGGCACTTTTCAACCCCTCTCCGGCCATGGGCGGATT 4091  
Db 1892 CTGGGCCAAGATCCAGAGACGGGGCGGCACTTTTCAACCCCTCTCCGGCCATGGGCGGATT 1941  
Qy 4092 CGGACTCAACACCAACCGCCATGATGCTCATCAAGAACACGCTGTGCCCGGAATAT 4151  
Db 1942 CGGACTCAACACCAACCGCCATGATGCTCATCAAGAACACGCTGTGCCCGGAATAT 2001  
Qy 4152 CACCAGCTTCTCGAGCTGCCGCTCAGAGTTCATCACCAGTACAGCACCGGCGAGGT 4211  
Db 2002 CACCAGCTTCTCGAGCTGCCGCTCAGAGTTCATCACCAGTACAGCACCGGCGAGGT 2061  
Qy 4212 CACCGTGGAGTGGAGTGGAGCTCAAGAGGAAACTTCAAGAGTGGAAACCCAGAGAT 4271  
Db 2062 CACCGTGGAGTGGAGTGGAGCTCAAGAGGAAACTTCAAGAGTGGAAACCCAGAGAT 2121  
Qy 4272 CCAGTACACAAACAACTACACACCCCGAGTTTGTGGACTTTTCCCGGACAGCACCGG 4331  
Db 2122 CCAGTACACAAACAACTACACACCCCGAGTTTGTGGACTTTTCCCGGACAGCACCGG 2181  
Qy 4332 GGAATACAGAACCAACAGACTTACGGAACCCGATACCTTACCGGACCCCTTTAACCCAT 4391  
Db 2182 GGAATACAGAACCAACAGACTTACGGAACCCGATACCTTACCGGACCCCTTTAACCCAT 2241

Qy 4392 TCATGTGCGCATACCTCAATAAA 4414  
Db 2242 TCATGTGCGCATACCTCAATAAA 2264

RESULT 10  
AX256328  
LOCUS AX256328 2264 bp DNA linear PAT 10-OCT-2001  
DEFINITION Sequence 8 from Patent WO0170276.  
ACCESSION AX256328  
VERSION AX256328.1 GI:16075185  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1

AUTHORS Chiorini, J. A., Kotin, R. M., Davidson, B. and Zabner, J.  
TITLE Aav5 vector for transducing brain cells and lung cells  
JOURNAL Patent: WO 0170276-A 8 27-SEP-2001;

The Secretary, Department of Health and Human Services (US);  
University of Iowa Research Foundation (US)

FEATURES  
source  
1. .2264  
Location/Qualifiers

/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="/Note = synthetic construct"

## ORIGIN

Query Match 46.9%; Score 2181.4; DB 6; Length 2264;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2232 TCAGATTTGGTGGAGAAAGTTGGTGAAGGTCTTCGCGAGTTTGGGCTTGAAGCGGG 2291  
Db 82 TCAAGATTTGGTGGAGAAAGTTGGTGAAGGTCTTCGCGAGTTTGGGCTTGAAGCGGG 141  
Qy 2292 CCACCCGAAACCAACCCATCAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCC 2351  
Db 142 CCACCCGAAACCAACCAACCCATCAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCTGCC 201  
Qy 2352 TGGTTATACTATCTCGGACCCGGAACCGGTCTCGATCGAGGAGAGCTGTCAACAGGGC 2411  
Db 202 TGGTTATACTATCTCGGACCCGGAACCGGTCTCGATCGAGGAGAGCTGTCAACAGGGC 261  
Qy 2412 AGACGAGTTCGCGGAGAGCAGACATCTCGTACACAGCAGCTTGAGCGGAGACAA 2471  
Db 262 AGACGAGTTCGCGGAGAGCAGACATCTCGTACACAGCAGCTTGAGCGGAGACAA 321  
Qy 2472 CCGCTACCTCAAGTACACCAACCGGACCGGAGTTTCAGGAGAGCTCCCGGACGAC 2531  
Db 322 CCGCTACCTCAAGTACACCAACCGGACCGGAGTTTCAGGAGAGCTCCCGGACGAC 381  
Qy 2532 ATCTCTCGGGGAAACCTTCGGAAGGCGAGTCTTTTCAGGCCAAGAAAAGGTTCTCGAAC 2591  
Db 382 ATCTCTCGGGGAAACCTTCGGAAGGCGAGTCTTTTCAGGCCAAGAAAAGGTTCTCGAAC 441  
Qy 2592 TTTTGGCTCGTTGAAGAGGTTGCTAAGACGGCCCTTACCGGAAAGCGGATAGACGACCA 2651  
Db 442 TTTTGGCTCGTTGAAGAGGTTGCTAAGACGGCCCTTACCGGAAAGCGGATAGACGACCA 501  
Qy 2652 CTTTCCAAAAGAAAGAGGCTCGGACCGGAGGACTTCAAGCCTTCCACCTCGTCAGA 2711  
Db 502 CTTTCCAAAAGAAAGAGGCTCGGACCGGAGGACTTCAAGCCTTCCACCTCGTCAGA 561  
Qy 2712 CGCGAAGCTGGACCCAGCGGATCCAGCAGCTGCAAAATCCAGCCCAACACGCTCAAG 2771  
Db 562 CGCGAAGCTGGACCCAGCGGATCCAGCAGCTGCAAAATCCAGCCCAACACGCTCAAG 621  
Qy 2772 TTTTGGAGCTGATACAAATGTCTCGGGAGGTGGCGCCATTTGGGGACAAATAACCAAG 2831  
Db 622 TTTTGGAGCTGATACAAATGTCTCGGGAGGTGGCGCCATTTGGGGACAAATAACCAAG 681

QY	2832	TGCGGATGAGTGGGCAATGCTCGGAGATTGGCAATTGCGATTCCACGTTGGATGGGGA	2891	QY	3912	GCAGATGGCCCAACAAACCAACAGAGTCCACACTGCTCCCGCGGACCGGACGCTACAACT	3971
Db	682	TGCGGATGAGTGGGCAATGCTCGGAGATTGGCAATTGCGATTCCACGTTGGATGGGGA	741	Db	1762	GCAGATGGCCCAACAAACCAACAGAGTCCACACTGCTCCCGCGGACCGGACGCTACAACT	1821
QY	2892	CAGAGTCGTACCAAGTCCACCGAACCTGGGTGCTGCCAGCTACAAACCAACACAGTA	2951	QY	3972	CCAGGAATTCGTCCCGGAGCGTGTGGATGAGAGGAGCTGTACTCTCAAGGACCCAT	4031
Db	742	CAGAGTCGTACCAAGTCCACCGAACCTGGGTGCTGCCAGCTACAAACCAACACAGTA	801	Db	1822	CCAGGAATTCGTCCCGGAGCGTGTGGATGAGAGGAGCTGTACTCTCAAGGACCCAT	1881
QY	2952	CGAGAGATCAAAAGCGGTCCGTGCAAGGAAGCAACGCAAGCCCTACTTTGGATACAG	3011	QY	4032	CTGGGCCAAGATCCCAAGACACGGGCGCACTTTACCCCTCTCCCGCCATGGGCGGATT	4091
Db	802	CGAGAGATCAAAAGCGGTCCGTGCAAGGAAGCAACGCAAGCCCTACTTTGGATACAG	861	Db	1882	CTGGGCCAAGATCCCAAGACACGGGCGCACTTTACCCCTCTCCCGCCATGGGCGGATT	1941
QY	3012	CACCCCTCGGGGTACTTTGACTTTAAACGCTTCCACAGCACTGGAGCCCGCGAGCTG	3071	QY	4092	CGGACTCAAAACACCCACCCCATGATGCTCATCAAGAACACGCTGTGCCGGAATAT	4151
Db	862	CACCCCTCGGGGTACTTTGACTTTAAACGCTTCCACAGCACTGGAGCCCGCGAGCTG	921	Db	1942	CGGACTCAAAACACCCACCCCATGATGCTCATCAAGAACACGCTGTGCCGGAATAT	2001
QY	3072	GCAAGACTCATCAACAACTACTGGGCTTCAGACCCCGGTCCCTCAGAGTCAAAATCTT	3131	QY	4152	CACGACTTCTCGGAGTCCCGGTGAGCAGCTTCATCCAGTACAGCACCGGCGAGT	4211
Db	922	GCAAGACTCATCAACAACTACTGGGCTTCAGACCCCGGTCCCTCAGAGTCAAAATCTT	981	Db	2002	CACGACTTCTCGGAGTCCCGGTGAGCAGCTTCATCCAGTACAGCACCGGCGAGT	2061
QY	3132	CACATTTCAAGTCAAAAGGTGACGCTGAGGACTCCACACCAACCATCGCCAAACCT	3191	QY	4212	CACCGTGGAGATGGAGTGGGAGCTCAAGAAAGGAAAACTCCAAGAGTGAACCCAGAGAT	4271
Db	982	CACATTTCAAGTCAAAAGGTGACGCTGAGGACTCCACACCAACCATCGCCAAACCT	1041	Db	2062	CACCGTGGAGATGGAGTGGGAGCTCAAGAAAGGAAAACTCCAAGAGTGAACCCAGAGAT	2121
QY	3192	CACCTCCACCGTCCAAAGTGTTTACGGACGACGACTACAGCTGCCCTACGTCGTGGGCAA	3251	QY	4272	CCAGTACACAAACAACTCAACGACCCCGAGTTTGTGGACTTTGCCCGGACAGACCGG	4331
Db	1042	CACCTCCACCGTCCAAAGTGTTTACGGACGACGACTACAGCTGCCCTACGTCGTGGGCAA	1101	Db	2122	CCAGTACACAAACAACTCAACGACCCCGAGTTTGTGGACTTTGCCCGGACAGACCGG	2181
QY	3252	CGGACCGAGGATGCTGCGGCTTCCCTCCGAGGTTTAAACGCTGCGGAGTACAGG	3311	QY	4332	GGATACAGAACACCAAGACCTATCGAAACCCGATACCTTACCCGACCCCTTTAAACCAT	4391
Db	1102	CGGACCGAGGATGCTGCGGCTTCCCTCCGAGGTTTAAACGCTGCGGAGTACAGG	1161	Db	2182	GGATACAGAACACCAAGACCTATCGAAACCCGATACCTTACCCGACCCCTTTAAACCAT	2241
QY	3312	TTACGCGAGCTGAAACCGGACACACAGAAATCCACCGAGGAGCAGCTTCTCTG	3371	QY	4392	TCATGTCGCATACCTCAATAAA	4414
Db	1162	TTACGCGAGCTGAAACCGGACACACAGAAATCCACCGAGGAGCAGCTTCTCTG	1221	Db	2242	TCATGTCGCATACCTCAATAAA	2264
QY	3372	CCTAGAGTACTTCCACAGCAAGTGTGTGAGAGGCAACAACTTTGAGTTTACCTACAA	3431	RESULT 11			
Db	1222	CCTAGAGTACTTCCACAGCAAGTGTGTGAGAGGCAACAACTTTGAGTTTACCTACAA	1281	AX256329			
QY	3432	CTTTGAGGAGTGCCTTCCACTCCAGCTTCGCTCCAGTCAGAACTGTTCAGCTGGC	3491	LOCUS	AX256329	2264 bp	DNA linear PAT 10-OCT-2001
Db	1282	CTTTGAGGAGTGCCTTCCACTCCAGCTTCGCTCCAGTCAGAACTGTTCAGCTGGC	1341	DEFINITION	Sequence 9 from Patent WO0170276.		
QY	3492	CAACCCGCTGGTGGACCACTGTGTACCGTTCGTGAGCACAATAAATACACTGCGGAGT	3551	ACCESSION	AX256329		
Db	1342	CAACCCGCTGGTGGACCACTGTGTACCGTTCGTGAGCACAATAAATACACTGCGGAGT	1401	VERSION	AX256329.1	GI:16075186	
QY	3552	CCAGTTCAACAAAGAACCTGGCGGGAGATACGCCAACACCTACAAAACTGGTTCCCGGG	3611	KEYWORDS	synthetic construct		
Db	1402	CCAGTTCAACAAAGAACCTGGCGGGAGATACGCCAACACCTACAAAACTGGTTCCCGGG	1461	SOURCE	synthetic construct		
QY	3612	GCCATGGGCGCAACCCAGGGCTGGAACTGGGGTCCGGGTCCACCGCCAGTGTACG	3671	ORGANISM	artificial sequences.		
Db	1462	GCCATGGGCGCAACCCAGGGCTGGAACTGGGGTCCGGGTCCACCGCCAGTGTACG	1521	REFERENCE	1		
QY	3672	CGCTTCGCCACCAACCAATAGGATGGAGTTCGAGGGCGGAGTTTACAGGTGCCCGGCA	3731	AUTHORS	Chiorini, J.A., Kolin, R.M., Davidson, B. and Zabner, J.		
Db	1522	CGCTTCGCCACCAACCAATAGGATGGAGTTCGAGGGCGGAGTTTACAGGTGCCCGGCA	1581	TITLE	Aav5 vector for transducing brain cells and lung cells		
QY	3732	GCCGAACGGCATGACCAACCACTCCAGGGCAGCAACACCTATGCCCTGGAGAACATAT	3791	JOURNAL	Patent: WO 0170276-A 9 27-SEP-2001;		
Db	1582	GCCGAACGGCATGACCAACCACTCCAGGGCAGCAACACCTATGCCCTGGAGAACATAT	1641		The Secretary, Department of Health and Human Services (US);		
QY	3792	GATCTTCAACAGCCAGCGCGGAACCCGGGACACCGCCAGCTACCTCGAGGCAACAT	3851	FEATURES	Location/Qualifiers		
Db	1642	GATCTTCAACAGCCAGCGCGGAACCCGGGACACCGCCAGCTACCTCGAGGCAACAT	1701	source	1. .2264		
QY	3852	GCTCATCAACAGGAGGAGAGACGACGCGGTGAACCGGCTGAGCTACAAACGTCGCGG	3911	/organism="synthetic construct"			
Db	1702	GCTCATCAACAGGAGGAGAGACGACGCGGTGAACCGGCTGAGCTACAAACGTCGCGG	1761	/mol type="unassigned DNA"			
				/db xref="taxon:32630"			
				/note="Note = synthetic construct"			
				ORIGIN			
				Query Match	46.9%;	Score 2181.4;	DB 6; Length 2264;
				Best Local Similarity	100.0%;	Pred. No. 0;	
				Matches 2182;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
QY	2232	TCAGATTTGTTGGAAGAAGTTGTTGAGGTCTTCGCGAGTTTTCGGGCTTGAAGCGG	2291				
Db	82	TCAGATTTGTTGGAAGAAGTTGTTGAGGTCTTCGCGAGTTTTCGGGCTTGAAGCGG	141				
QY	2292	CCCACCGAAACCAAAACCCCAATCAGACGATCAAGATCAAGCCCGTGTCTTGTGCTGCC	2351				
Db	142	CCCACCGAAACCAAAACCCCAATCAGACGATCAAGATCAAGCCCGTGTCTTGTGCTGCC	201				



Qy	2352	TGTTTAAACTATCTCGAACCGCGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGC	2411
Db	202	TGGTTATAACTATCTCGAACCGCGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGC	261
Qy	2412	AGACGAGGTCGCGGAGAGCAGCATCTCGTACAAAGCAGCAGCTTCAGGCGGGAGCAAA	2471
Db	262	AGACGAGGTCGCGGAGAGCAGCATCTCGTACAAAGCAGCAGCTTCAGGCGGGAGCAAA	321
Qy	2472	CCCTTACTCTCAAGTACAAACCAACGCGGACGCGAGTTCAGGAGAAGCTCGCCGACGACAC	2531
Db	322	CCCTTACTCTCAAGTACAAACCAACGCGGACGCGAGTTCAGGAGAAGCTCGCCGACGACAC	381
Qy	2532	ATCCTTCGGGGGAAACCTCGGAAAGGCAGTCTTTTCAGGCCAAGAAAAAGGTTCTCGAACC	2591
Db	382	ATCCTTCGGGGGAAACCTCGGAAAGGCAGTCTTTTCAGGCCAAGAAAAAGGTTCTCGAACC	441
Qy	2592	TTTTGGGCTGGTTGAAAGGGTGCTAAGACGGGCCCTTACCGGAAGCGGATAGACGACCA	2651
Db	442	TTTTGGGCTGGTTGAAAGGGTGCTAAGACGGGCCCTTACCGGAAGCGGATAGACGACCA	501
Qy	2652	CTTTTCCAAAAAGAAAGAGGCTCGAACCGAAGAGACTTCCAAGCCTTCCACCTCGTCAGA	2711
Db	502	CTTTTCCAAAAAGAAAGAGGCTCGAACCGAAGAGACTTCCAAGCCTTCCACCTCGTCAGA	561
Qy	2712	CGCGAAGCTGGACCCAGCGGATCCCAAGCACTGCAAAATCCAGCCCAACCAAGCCTCAAG	2771
Db	562	CGCGAAGCTGGACCCAGCGGATCCCAAGCACTGCAAAATCCAGCCCAACCAAGCCTCAAG	621
Qy	2772	TTTTGGGAGCTGATACATATGCTCGGGAGAGGTGGGGGCCCATTTGGGCGACAATATCAAGG	2831
Db	622	TTTTGGGAGCTGATACATATGCTCGGGAGAGGTGGGGGCCCATTTGGGCGACAATATCAAGG	681
Qy	2832	TGCCGATGGAGTGGGCAATGCTCGGAGATTTGGCATTTGGCATTCACGTGGATGGGGGA	2891
Db	682	TGCCGATGGAGTGGGCAATGCTCGGAGATTTGGCATTTGGCATTCACGTGGATGGGGGA	741
Qy	2892	CAGAGTCGTCAACCAAGTCCACCGCAACCTCGGTGCTGCCAGCTACAAACCAACCAAGTA	2951
Db	742	CAGAGTCGTCAACCAAGTCCACCGCAACCTCGGTGCTGCCAGCTACAAACCAACCAAGTA	801
Qy	2952	CCGAGAGATCAAAAGCGGCTCCGTGAGCGGAAGCAACGCCAAGCCCTACTTTGGATACAG	3011
Db	802	CCGAGAGATCAAAAGCGGCTCCGTGAGCGGAAGCAACGCCAAGCCCTACTTTGGATACAG	861
Qy	3012	CACCCCTCGGGGTACTTTGACTTTAACCGCTTCCACAGCCACTGGAGCCCCCGAGACTG	3071
Db	862	CACCCCTCGGGGTACTTTGACTTTAACCGCTTCCACAGCCACTGGAGCCCCCGAGACTG	921
Qy	3072	GCAAAAGTCAATCAAACTACTGGGCTTTAGACCCCGGTCCTCAGAGTCAAAATCTTT	3131
Db	922	GCAAAAGTCAATCAAACTACTGGGCTTTAGACCCCGGTCCTCAGAGTCAAAATCTTT	981
Qy	3132	CAACATTCAGTCAAGTCAAGTTCAGGACGACACTACACAGTCCGCTACGCAACCACTT	3191
Db	982	CAACATTCAGTCAAGTTCAGGACGACACTACACAGTCCGCTACGCAACCACTT	1041
Qy	3192	CACCTCCACCGTCCAAGTGTTCAGGACGACACTACACAGTCCGCTACGCTCGTGGCAA	3251
Db	1042	CACCTCCACCGTCCAAGTGTTCAGGACGACACTACACAGTCCGCTACGCTCGTGGCAA	1101
Qy	3252	CGGACCGAGGATGCTTCGCGGCTTCCCTCGCAGGTCTTTACGCTCGCGAGTACGG	3311
Db	1102	CGGACCGAGGATGCTTCGCGGCTTCCCTCGCAGGTCTTTACGCTCGCGAGTACGG	1161
Qy	3312	TTACGCAACGCTGAACCGCGACAAACAGAAAAATCCACCGAGAGGAGCTTCTCTG	3371
Db	1162	TTACGCAACGCTGAACCGCGACAAACAGAAAAATCCACCGAGAGGAGCTTCTCTG	1221
Qy	3372	CCTAGAGTACTTTCCCGCAGAGATGCTTGAGAAAGGGCAACAACTTTTACGTACCTCAA	3431
Db	1222	CCTAGAGTACTTTCCCGCAGAGATGCTTGAGAAAGGGCAACAACTTTTACGTACCTCAA	1281
Qy	3432	CTTTGAGGAGGTGCCCTTCCACTCCAGCTTCGCTCCCAAGTCCAGAACCTGTTCAAGCTGGC	3491

1282	Db	CTTTGAGAGGTGCCCTTCCACTCCAGCTTCGCTCCAGTCCAGAACCTGTTCAAGCTGGC	1341
3492	Qy	CAACCCGCTGTTGGACCAAGTACTTGTACCGCTTCTGTGAGCACAAATAACACTCGCGGAGT	3551
1342	Db	CAACCCGCTGTTGGACCAAGTACTTGTACCGCTTCTGTGAGCACAAATAACACTCGCGGAGT	1401
3552	Qy	CCAGTTCAAAAGAAACCTGSCCGGGAGATACGCCAACACCTACAAAACCTGGTTCOCGGG	3611
1402	Db	CCAGTTCAAAAGAAACCTGSCCGGGAGATACGCCAACACCTACAAAACCTGGTTCOCGGG	1461
3612	Qy	GCCATGGGCGGRACCCAGGGCTGGACCTGGCTTCGGGGTCAACCGCGCAGTGTACG	3671
1462	Db	GCCATGGGCGGAAACCCAGGGCTGGAACTTGGGCTTCGGGGTCAACCGCGCAGTGTACG	1521
3672	Qy	CGCCTTCGCCACGACCAATAGGATGGAGCTCGAGGGCGCGAGTTACCCAGTGGCCCCGCCA	3731
1522	Db	CGCCTTCGCCACGACCAATAGGATGGAGCTCGAGGGCGCGAGTTACCCAGTGGCCCCGCCA	1581
3732	Qy	GCCGAACGGCTGACCAACAACTCCAGGGCAGCAACCTATGCTTGGAGACACTAT	3791
1582	Db	GCCGAACGGCTGACCAACAACTCCAGGGCAGCAACCTATGCTTGGAGACACTAT	1641
3792	Qy	GATCTTCAAGAGCAGCGCGCGAAACCCGGGCAACACGCCACAGTACCTCGAGGGCAACAT	3851
1642	Db	GATCTTCAAGAGCAGCGCGGAAACCCGGGCAACACGCCACAGTACCTCGAGGGCAACAT	1701
3852	Qy	GCTCATCAAGCGAGAGCGAGACGACGCGGTGAACCGCGTGGCGTACAACTCGCGCGG	3911
1702	Db	GCTCATCAAGCGAGAGCGAGACGACGCGGTGAACCGCGTGGCGTACAACTCGCGCGG	1761
3912	Qy	GCAGATGCGCACCAACAAACAGAGCTCCACCTGCTGCCCGCGACCGGACGTACAACT	3971
1762	Db	GCAGATGCGCACCAACAAACAGAGCTCCACCTGCTGCCCGCGACCGGACGTACAACT	1821
3972	Qy	CCAGGAAATCGTGCCTCGCGACGCGTGTGGATGGAGAGGACGCTGACTTCCAGGAGCCAT	4031
1822	Db	CCAGGAAATCGTGCCTCGCGACGCGTGTGGATGGAGAGGACGCTGACTTCCAGGAGCCAT	1881
4032	Qy	CTGGGCGAAGTCCCAGAGAGGGGGCGCACTTTCACCTCTCCGSCCATGGCGGAT	4091
1882	Db	CTGGGCGAAGTCCCAGAGAGGGGGCGCACTTTCACCTCTCCGSCCATGGCGGAT	1941
4092	Qy	CGGACTCAAAACACCCACCGCCCATGATGCTCATCAAGAAACGCGCTGTGCCCGAAATAT	4151
1942	Db	CGGACTCAAAACACCCACCGCCCATGATGCTCATCAAGAAACGCGCTGTGCCCGAAATAT	2001
4152	Qy	CACAGCTTCTCGAGCGTGGCGGTACAGACGCTTCATCACCAGTACAGCACCGGGCAGGT	4211
2002	Db	CACAGCTTCTCGAGCGTGGCGGTACAGACGCTTCATCACCAGTACAGCACCGGGCAGGT	2061
4212	Qy	CACCGTGGAGTGGAGTGGGAGCTCAAGAGAGAAACTCCACAGAGTGGAAACCCAGAGAT	4271
2062	Db	CACCGTGGAGTGGAGTGGGAGCTCAAGAGAGAAACTCCACAGAGTGGAAACCCAGAGAT	2121
4272	Qy	CCAGTACACAAACCTACAAAGACCCCGAGTTGTGGACTTTTGCCCGGACAGCACCGG	4331
2122	Db	CCAGTACACAAACCTACAAAGACCCCGAGTTGTGGACTTTTGCCCGGACAGCACCGG	2181
4332	Qy	GGAATACAGAACCAACAGACTTACGGAACCCGATACCTTACCGGACCCCTTTAAACCCAT	4391
2182	Db	GGAATACAGAACCAACAGACTTACGGAACCCGATACCTTACCGGACCCCTTTAAACCCAT	2241
4392	Qy	TCATGTCGCATACCTCAATAAA	4414
2242	Db	TCATGTCGCATACCTCAATAAA	2264

RESULT 12			
BD211186			
LOCUS	BD211186	1870 bp	DNA
DEFINITION	AAV5 vector and uses thereof.		
ACCESSION	BD211186		
			linear
			PAT 17-JUL-2003

BD211186.1 GI:33020956  
KEYWORDS JP 2002516092-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1. (bases 1 to 1870)  
AUTHORS Chlorini, J.A. and Kotin, R.M.  
TITLE AAV5 vector and uses thereof  
JOURNAL Patent: JP 2002516092-A 6 04-JUN-2002;  
THE UNITED STATES OF AMERICA  
COMMENT OS Artificial Sequence  
EN JP 2002516092-A/6  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000550986  
PR 28-MAY-1998 US 60/087029  
PI JOHN A. CHLORINI, ROBERT M. KOTIN  
PC C12N15/09, C07K14/015, C07K16/08, C12N7/00, C12Q1/68, G01N33/15, PC  
G01N33/50,  
PC C12N15/00  
CC Description of Artificial Sequence: (Note = synthetic construct  
FH Key Location/Qualifiers  
FT source 1..1870  
FT /organism='Artificial Sequence'.  
Location/Qualifiers  
1..1870  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

Query Match 40.2%; Score 1870; DB 6; Length 1870;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 327 ATTCCTTGTCTCGAGCTGTAGAGGACCCCTCGCTGCCATGGCTACCTTCTATGAAGTCAT 386  
DB 1 ATTCCTTGTCTCGAGCTGTAGAGGACCCCTCGCTGCCATGGCTACCTTCTATGAAGTCAT 60

QY 387 TGTTCGCGTCCCATTTGACGTGGAGGAACATCTGCTGGGAATTTCTGACAGCTTTGTGGA 446  
DB 61 TGTTCGCGTCCCATTTGACGTGGAGGACATCTGCTGGAAATTTCTGACAGCTTTGTGGA 120

QY 447 CTGGTAACGTGCAAAATTTGGAGCTGCTCCAGAGTCAGATTTAAATTTGACTCTGGT 506  
DB 121 CTGGTAACGTGCAAAATTTGGAGCTGCTCCAGAGTCAGATTTAAATTTGACTCTGGT 180

QY 507 TGAACAGCTCAGTTGACCGTGGCTGATAGAAATTCGCGCGTCTTCTGTACGAGTGAA 566  
DB 181 TGAACAGCTCAGTTGACCGTGGCTGATAGAAATTCGCGCGTCTTCTGTACGAGTGAA 240

QY 567 CAAATTTTCCAGCAGAGTCCAAATTTCTTTGTGCAAGTTTGAAGGGATCTGAATATTT 626  
DB 241 CAAATTTTCCAGCAGAGTCCAAATTTCTTTGTGCAAGTTTGAAGGGATCTGAATATTT 300

QY 627 TCATCTGCACACGCTTGTGGAGACCTCGGCAATCTCTTCCATCGTCTCTCGGCGCTACGT 686  
DB 301 TCATCTGCACACGCTTGTGGAGACCTCGGCAATCTCTTCCATCGTCTCTCGGCGCTACGT 360

QY 687 GAGTCAGATTCGCGCCAGCTGTGAAGTGTCTTCCAGGGAATTCACCCAGATCAA 746  
DB 361 GAGTCAGATTCGCGCCAGCTGTGAAGTGTCTTCCAGGGAATTCACCCAGATCAA 420

QY 747 CGACTGGGTGCGCATCACCAAGTAAAGAGGCGGAGGCAATAAGTGTGGATTTCTGG 806  
DB 421 CGACTGGGTGCGCATCACCAAGTAAAGAGGCGGAGGCAATAAGTGTGGATTTCTGG 480

QY 807 GTATATTCGCGCTACCTGCTGCCGAAGTTCACCGAGCTTCAGTGGCGGTGGACAA 866  
DB 481 GTATATTCGCGCTACCTGCTGCCGAAGTTCACCGAGCTTCAGTGGCGGTGGACAA 540

QY 867 CCTGGACGAGTATAAATTTGCGCGCTCTGAATCTGGAGGAGCGCAACCGCTCTCGCGCA 926  
DB 541 CCTGGACGAGTATAAATTTGCGCGCTCTGAATCTGGAGGAGCGCAACCGCTCTCGCGCA 600

QY 927 GTTTCTGGCAGAAATCTCGCAGCGCTCGCAGGAGGCGGCTTCGCACGCTGAGTTCCTCGG 986  
DB 601 GTTTCTGGCAGAAATCTCGCAGCGCTCGCAGGAGGCGGCTTCGCACGCTGAGTTCCTCGG 660

QY 987 TGACCCGGTCACTCAAAGCAAGACTTCCAGAAATACATGGCGCTCGTCAACTGGCTCGT 1046  
DB 661 TGACCCGGTCACTCAAAGCAAGACTTCCAGAAATACATGGCGCTCGTCAACTGGCTCGT 720

QY 1047 GGAGCAGCGCATCACTTCGAGAGCAGTGGATCCAGGAAATCAGAGAGCTACCTCTC 1106  
DB 721 GGAGCAGCGCATCACTTCGAGAGCAGTGGATCCAGGAAATCAGAGAGCTACCTCTC 780

QY 1107 CTTTCAACTCCACCGGCAACTCTCGAGAGCCAGATCAAGGCGCGCTCGAACCGGACCAA 1166  
DB 781 CTTTCAACTCCACCGGCAACTCTCGAGAGCCAGATCAAGGCGCGCTCGAACCGGACCAA 840

QY 1167 AATTATGATCTGACAAAAAGCGCGGTGAGTACCTCGTGGGAGTCTCGTTCGAGGA 1226  
DB 841 AATTATGATCTGACAAAAAGCGCGGTGAGTACCTCGTGGGAGTCTCGTTCGAGGA 900

QY 1227 CATTTCAAAAACAGAAATCTGGCAATTTTGGAGATGAATGGCTAGCAGCCGCGCTACGC 1286  
DB 901 CATTTCAAAAACAGAAATCTGGCAATTTTGGAGATGAATGGCTAGCAGCCGCGCTACGC 960

QY 1287 GGGATCCATCTCTACGGCTGGTGTGAGCGCTCTTCAACAAGAGGAAACACCGCTCTGGCT 1346  
DB 961 GGGATCCATCTCTACGGCTGGTGTGAGCGCTCTTCAACAAGAGGAAACACCGCTCTGGCT 1020

QY 1347 CTACGGACCCGGCACGACCGGCAAGACCAACTCGCGGAGGCGCATCCGACACTGTGCC 1406  
DB 1021 CTACGGACCCGGCACGACCGGCAAGACCAACTCGCGGAGGCGCATCCGACACTGTGCC 1080

QY 1407 CTTTTCACGCTCGGTGAACTGGACCAATGAAACTTTCCCTTTAAAGTCTGTGTGACAA 1466  
DB 1081 CTTTTCACGCTCGGTGAACTGGACCAATGAAACTTTCCCTTTAAAGTCTGTGTGACAA 1140

QY 1467 AATGCTCATTTTGGTGGAGGAGGAAAGATGACCAACAAGGTGGTGAATCCGCCAAGGC 1526  
DB 1141 AATGCTCATTTTGGTGGAGGAGGAAAGATGACCAACAAGGTGGTGAATCCGCCAAGGC 1200

QY 1527 CATCTCGGGGGCTCAAGGTGGGGTGCATCAGAAATGTAATCTCTGTTCAAAATGGA 1586  
DB 1201 CATCTCGGGGGCTCAAGGTGGGGTGCATCAGAAATGTAATCTCTGTTCAAAATGGA 1260

QY 1587 TTCTACCCCTGTCAATTGTAACCTTCCAATACAAACATGTGTGTGCTGTGATGGGAATTC 1646  
DB 1261 TTCTACCCCTGTCAATTGTAACCTTCCAATACAAACATGTGTGTGCTGTGATGGGAATTC 1320

QY 1647 CACGACCTTTGAAACACACGACGCGCTGGAGGACCGCATGTTCAAATTTGAACTGACTAA 1706  
DB 1321 CACGACCTTTGAAACACACGACGCGCTGGAGGACCGCATGTTCAAATTTGAACTGACTAA 1380

QY 1707 GGGGCTCCGCGCAGATTTGGCAGAGTACTAGCAGGAGTCAAGGACTTTTTCGTTG 1766  
DB 1381 GGGGCTCCGCGCAGATTTTGGCAGAGTACTAGCAGGAGTCAAGGACTTTTTCGTTG 1440

QY 1767 GGCAGAGGTCAATCAGGTGCGGTGACTCAGAGTTTAAAGTTTCCAGGGAATTCGCGGG 1826  
DB 1441 GGCAGAGGTCAATCAGGTGCGGTGACTCAGAGTTTAAAGTTTCCAGGGAATTCGCGGG 1500

QY 1827 AACTAAAGGGGGGAGAAATCTCTAAACGCCACTGGGTGAGCTGCCAATACTAGCTA 1886  
DB 1501 AACTAAAGGGGGGAGAAATCTCTAAACGCCACTGGGTGAGCTGCCAATACTAGCTA 1560

QY 1887 TAAAGTCTGGAGAGCGGCGCAGGCTCTCATTTGTTCCGAGACCGCTCGAGTTTCA 1946  
DB 1561 TAAAGTCTGGAGAGCGGCGCAGGCTCTCATTTGTTCCGAGACCGCTCGAGTTTCA 1620

QY 1947 CGTGACTGTTGATCCCGCTCTCTGCGACCGGTCAATTTGGAATTTCAAGGTATGATTCGCA 2006  
DB 1621 CGTGACTGTTGATCCCGCTCTCTGCGACCGGTCAATTTGGAATTTCAAGGTATGATTCGCA 1680

QY	2007	ATGTGACTATCATGCTCAATTTGTGACAACTTTCTAAACAAATGTGATGAATGTGAATATTT	2066
DB	1681	ATGTGACTATCATGCTCAATTTGTGACAACTTTCTAAACAAATGTGATGAATGTGAATATTT	1740
QY	2067	GAATCGGGGCAAAATGTGATCTATCTGTCAAAATGTAACCTCACTGTCAAAATTTGTCTATGG	2126
DB	1741	GAATCGGGGCAAAATGTGATCTATCTGTCAAAATGTAACCTCACTGTCAAAATTTGTCTATGG	1800
QY	2127	GATTCCCCCTCGGAAAGGAAAACTTTGTGAGATTTTGGGGAATTTTGCAGATGCCAATAA	2186
DB	1801	GATTCCCCCTCGGAAAGGAAAACTTTGTGAGATTTTGGGGAATTTTGCAGATGCCAATAA	1860
QY	2187	AGAACAGTAA	2196
DB	1861	AGAACAGTAA	1870
RESULT 13			
AX256331			
LOCUS	AX256331	1870 bp	DNA
DEFINITION	Sequence 11 from Patent WO0170276.		linear
ACCESSION	AX256331		PAT 10-OCT-2001
VERSION	AX256331.1	GI:16075188	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
	artificial sequences.		
REFERENCE	1		
AUTHORS	Chiorini, J.A., Kotin, R.M., Davidson, B. and Zabner, J.		
TITLE	Aav5 vector for transducing brain cells and lung cells		
JOURNAL	Patent: WO 0170276-A 11 27-SEP-2001;		
	The Secretary, Department of Health and Human Services (US) ;		
	University of Iowa Research Foundation (US)		
FEATURES	Location/Qualifiers		
source	1..1870		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Note = synthetic construct"		
ORIGIN			
Query Match	40.2%	Score 1870;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 0;	Length 1870;
Matches 1870;	Conservative	0;	Mismatches 0;
		Indels	0;
		Gaps	0;
QY	327	ATTCTTTGCTCTGGACTGCTAGAGACCCCTCGCTGCCATGGCTACCTTCTATGAAGTCAT	386
DB	1	ATTCTTTGCTCTGGACTGCTAGAGACCCCTCGCTGCCATGGCTACCTTCTATGAAGTCAT	60
QY	387	TGTTTCGGTCCCATTTGACGTGAGAGAACTCTGCCCTGGAAATTTCTGACAGCTTTGTGA	446
DB	61	TGTTTCGGTCCCATTTGACGTGAGAGAACTCTGCCCTGGAAATTTCTGACAGCTTTGTGA	120
QY	447	CTGGGTAACTGGTCAAAATTTGGGAGCTGCCTCCAGAGTCAGATTTTAAATTTGACTCTGGT	506
DB	121	CTGGGTAACTGGTCAAAATTTGGGAGCTGCCTCCAGAGTCAGATTTTAAATTTGACTCTGGT	180
QY	507	TGAACAGCCTCAGTTCACCGTGGCTGATAGAAATTCGCCCGCTGTTCCCTGACAGTGGAA	566
DB	181	TGAACAGCCTCAGTTCACCGTGGCTGATAGAAATTCGCCCGCTGTTCCCTGACAGTGGAA	240
QY	567	CAAAATTTCCACAGGAGTCCAAATTTCTTTGTGCAAGTTTGAAGGGATCTGAATATTT	626
DB	241	CAAAATTTCCACAGGAGTCCAAATTTCTTTGTGCAAGTTTGAAGGGATCTGAATATTT	300
QY	627	TCACTGCAACAGCTTTGTGGAGACCTCCGCACTCTCTCCATGCTCCTCGGCCGTACGT	686
DB	301	TCACTGCAACAGCTTTGTGGAGACCTCCGCACTCTCTCCATGCTCCTCGGCCGTACGT	360
QY	687	GAGTCAGATTCGCCCCAGCTGGTGAAGTGGTCTTCCAGGGAATTGAACCCAGATCAA	746
DB	361	GAGTCAGATTCGCCCCAGCTGGTGAAGTGGTCTTCCAGGGAATTGAACCCAGATCAA	420

1501 AACTAAGGGCGGAGAAATCTCTAAAGCCCACTGGGTGACGTCACCAATACTAGCTA 1560  
1887 TAAAGTCTGGAGAGCGGGCCAGGCTCTCAATTTGTTCCGAGAGAGCGCTCGAGTTTCA 1946  
1561 TAAAGTCTGGAGAGCGGGCCAGGCTCTCAATTTGTTCCGAGAGAGCGCTCGAGTTTCA 1620  
1947 CGTGACTGTGATCCCGCTCTCTCGACCGCTCAATTTGGAATTCAGAGTATGATTTGCAA 2006  
1621 CGTGACTGTGATCCCGCTCTCTCGACCGCTCAATTTGGAATTCAGAGTATGATTTGCAA 1680  
2007 ATGTGACTATCATGTCTCAATTTGACAAACATTTCTAAACAAATGTGATGAATTTT 2066  
1681 ATGTGACTATCATGTCTCAATTTGACAAACATTTCTAAACAAATGTGATGAATTTT 1740  
2067 GAATCGGGGCAAAATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 2126  
1741 GAATCGGGGCAAAATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 1800  
2127 GATTTCCCTCTGGGAAAGGAAATTTGTCAGATTTTGGGATTTTGAAGTCCCAATAA 2186  
1801 GATTTCCCTCTGGGAAAGGAAATTTGTCAGATTTTGGGATTTTGAAGTCCCAATAA 1860  
2187 AGAACAGTAA 2196  
1861 AGAACAGTAA 1870  
RESULT 14  
AX496951  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
ORIGIN  
Query Match 39.4%; Score 1833; DB 6; Length 1833;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
364 ATGGCTACCTTCTATGAAGTCAATTTGCGGTCCCATTTGACGTGGAGGAACATCTGCCT 423  
1 ATGGCTACCTTCTATGAAGTCAATTTGCGGTCCCATTTGACGTGGAGGAACATCTGCCT 60  
424 GGAATTTCTGACAGCTTTGTGGACTGGGTAACTGGTCAAAATTTGGGAGCTGCTCCAGAG 483  
61 GGAATTTCTGACAGCTTTGTGGACTGGGTAACTGGTCAAAATTTGGGAGCTGCTCCAGAG 120  
484 TCAGATTTAAATTTGACTCTGTTTGAACAGCTCAGTTGACGTTGCGGTGCTGATAGATTCGC 543  
121 TCAGATTTAAATTTGACTCTGTTTGAACAGCTCAGTTGACGTTGCGGTGCTGATAGATTCGC 180  
544 CGCGTGTTCCTGTACGAGTGAACAAATTTTCCAGCAGGAGTCCAAATTTCTTTGTGCAG 603  
181 CGCGTGTTCCTGTACGAGTGAACAAATTTTCCAGCAGGAGTCCAAATTTCTTTGTGCAG 240  
604 TTTGAAAGGGATCTGAATATTTTCACTGTGACAGCTTTGGAGAGCTCCGGATCTCT 663

241 TTTGAAAGGGATCTGAATATTTTTCATCTGACACGCTTGTGGAGACCTCCGCACTCTCT 300  
664 TCCATGGTCTCTCGCGCGCTACGTGAGTCAGATTCGCGGCCAGCTGGTGAAGTGGTCTTC 723  
301 TCCATGGTCTCTCGCGCGCTACGTGAGTCAGATTCGCGGCCAGCTGGTGAAGTGGTCTTC 360  
724 CAGGGAATTTGAACCCAGATCAACGACTGGGTGCGCATCACCAAGGTAAAGAGGGCGGA 783  
361 CAGGGAATTTGAACCCAGATCAACGACTGGGTGCGCATCACCAAGGTAAAGAGGGCGGA 420  
784 GCAATTAAGTGGTGGATCTGGGTATATTCGCGCTACTCTGCGCAAGTCCCAACCG 843  
421 GCAATTAAGTGGTGGATCTGGGTATATTCGCGCTACTCTGCGCAAGTCCCAACCG 480  
844 GAGCTTCAGTGGCGCTGGACAAACCTGGACGAGTATAAATTTGGCCGCCCTGAATCTGGAG 903  
481 GAGCTTCAGTGGCGCTGGACAAACCTGGACGAGTATAAATTTGGCCGCCCTGAATCTGGAG 540  
904 GAGCGCAAACGGCTCGTCCGCGAGTTTCTGGGAGAAATCTCGCAGCGCTCGCAGGAGCG 963  
541 GAGCGCAAACGGCTCGTCCGCGAGTTTCTGGGAGAAATCTCGCAGCGCTCGCAGGAGCG 600  
964 GCTTCGACGCTGAGTTCTCGGCTGACCCGCTCATCAAAAGCAAGACTTCCCAAGAAATAC 1023  
601 GCTTCGACGCTGAGTTCTCGGCTGACCCGCTCATCAAAAGCAAGACTTCCCAAGAAATAC 660  
1024 ATGGCGCTCTCAACTGGCTCGTGGAGCAACGCTCATCTTCCGAGAAAGAGTGGATCCAG 1083  
661 ATGGCGCTCTCAACTGGCTCGTGGAGCAACGCTCATCTTCCGAGAAAGAGTGGATCCAG 720  
1084 GAAATCAGAGAGTACCTCTCTTCAACTCCACCGGCAACTCTCGAGCCAGATCAAG 1143  
721 GAAATCAGAGAGTACCTCTCTTCAACTCCACCGGCAACTCTCGAGCCAGATCAAG 780  
1144 GCGCGCTCGAACAACCGGACCAAAATTTAGTGTCTGACAAAAGAGCGGTGGACTACCTC 1203  
781 GCGCGCTCGAACAACCGGACCAAAATTTAGTGTCTGACAAAAGAGCGGTGGACTACCTC 840  
1204 GTGGGAGCTCTCCGCGAGCAATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGATG 1263  
841 GTGGGAGCTCTCCGCGAGCAATTTCAAAAACAGAAATCTGGCAAAATTTTGGAGATG 900  
1264 AATGGCTACGACCCCGCTACGCGGATCCATCTCTACGCGCTGGTGTACGCGCTCTCTC 1323  
901 AATGGCTACGACCCCGCTACGCGGATCCATCTCTACGCGCTGGTGTACGCGCTCTCTC 960  
1324 AACAGAGGAGCAACCGCTCTGCGCTACGAGCCCGCACGACCGGCAAGCAACATCGCG 1383  
961 AACAGAGGAGCAACCGCTCTGCGCTACGAGCCCGCACGACCGGCAAGCAACATCGCG 1020  
1384 GAGGCCATCGCCACACTGTGCCCTTTTACGGCTGGTGAATCTGGACCAATGAAACTTT 1443  
1021 GAGGCCATCGCCACACTGTGCCCTTTTACGGCTGGTGAATCTGGACCAATGAAACTTT 1080  
1444 CCCTTTAATGACTGTGTGACAAATGCTCAATTTGGTGGAGGAGGAAAGATGACCAAC 1503  
1081 CCCTTTAATGACTGTGTGACAAATGCTCAATTTGGTGGAGGAGGAAAGATGACCAAC 1140  
1504 AAGTGTGTAATCCGCAAGGCGCATCTGGGGGCTCAAAAGGTGCGGGTCAATGACAAA 1563  
1141 AAGTGTGTAATCCGCAAGGCGCATCTGGGGGCTCAAAAGGTGCGGGTCAATGACAAA 1200  
1564 TGTAAATCTCTGTTCAAATTTGATTTACCCCTGTCAATTTGATTTTCAATCAAAATG 1623  
1201 TGTAAATCTCTGTTCAAATTTGATTTTACCCCTGTCAATTTGATTTTCAATCAAAATG 1260  
1624 TGTGTGTGTGTGATGGGAATTCAGACCTTTGAACACGAGCGCGCTGGAGGACCG 1683  
1261 TGTGTGTGTGTGATGGGAATTCAGACCTTTGAACACGAGCGCGCTGGAGGACCG 1320  
1684 ATGTTCAAAATTTGAACCTGACTTAAGCGGCTCCCGCAGATTTTGGCAAGATTTACTAAG 1743  
1321 ATGTTCAAAATTTGAACCTGACTTAAGCGGCTCCCGCAGATTTTGGCAAGATTTACTAAG 1380

```

QY 1744 GAAGTCAAGGACTTTTGGTGGCGGCAAGGTCAATCAGGTGCGGTGACTCAACGAGTTT 1803
Db 1381 GAAGTCAAGGACTTTTGGTGGCGGCAAGGTCAATCAGGTGCGGTGACTCAACGAGTTT 1440
QY 1804 AAAGTTCCCGAGGAATGGCGGGAACCTAAGGGGCGGAGAAATCTCTAAAACGCCCACTG 1863
Db 1441 AAAGTTCCCGAGGAATGGCGGGAACCTAAGGGGCGGAGAAATCTCTAAAACGCCCACTG 1500
QY 1864 GTGAGCTCACCAATACTAGCTATAAAAGTCTGAGAAGCGGGCCAGGCTCTCATTTGTT 1923
Db 1501 GGTGAGCTCACCAATACTAGCTATAAAAGTCTGAGAAGCGGGCCAGGCTCTCATTTGTT 1560
QY 1924 CCGGAGCGCTCGCAGTTTCAGAGTGAATGTTGATCCCGCTCTCTGGAGCGGTCAAT 1983
Db 1561 CCGGAGCGCTCGCAGTTTCAGAGTGAATGTTGATCCCGCTCTCTGGAGCGGTCAAT 1620
QY 1984 TGGAAATCAAGGTATGATTGCAAACTGACTATCATCTCAATTTGACAAATTTCTAAC 2043
Db 1621 TGGAAATCAAGGTATGATTGCAAACTGACTATCATCTCAATTTGACAAATTTCTAAC 1680
QY 2044 AAATGTGATGAATGTAATTTGAATCGGGGCAAAATATGATGATCTGTCAATGTA 2103
Db 1681 AAATGTGATGAATGTAATTTGAATCGGGGCAAAATATGATGATCTGTCAATGTA 1740
QY 2104 ACTCACTGTCAATTTGATGGAATTCCTCCCTGGGAAAGGAAATCTGTGAGATTT 2163
Db 1741 ACTCACTGTCAATTTGATGGAATTCCTCCCTGGGAAAGGAAATCTGTGAGATTT 1800
QY 2164 GGGGATTTTGAGTGCATGCAATTAAGCAAGTAA 2196
Db 1801 GGGGATTTTGAGTGCATGCAATTAAGCAAGTAA 1833

RESULT 15
AX703460
LOCUS AX703460 1833 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 22 from Patent WO02066653.
ACCESSION AX703460
VERSION AX703460.1 GI:29539437
KEYWORDS
SOURCE Adeno-associated virus 5
ORGANISM Adeno-associated virus 5
REFERENCE 1
AUTHORS Li, M. and Liu, Y. C.
TITLE Procarotytic libraries and uses
JOURNAL Patent: WO 02066653-A 22 29-AUG-2002;
Xencor (US)
FEATURES
    source      Location/Qualifiers
    1..1833
    /organism="Adeno-associated virus 5"
    /mol_type="unassigned DNA"
    /db_xref="taxon:82300"

ORIGIN
Query Match 39.4%; Score 1833; DB 6; Length 1833;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 ATGGCTACCTTCATGAAGTCATTGTTCGGTCCCATTTGACGTGGAGGAACATCTGCCT 423
Db 1 ATGGCTACCTTCATGAAGTCATTGTTCGGTCCCATTTGACGTGGAGGAACATCTGCCT 60
QY 424 GGAATTTCTGACAGCTTTGTGGACTGGGTAACTGGTCAAAATTTGGGAGCTGCCTCCAGAG 483
Db 61 GGAATTTCTGACAGCTTTGTGGACTGGGTAACTGGTCAAAATTTGGGAGCTGCCTCCAGAG 120
QY 484 TCAGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGGCTGATGAATTCGC 543
Db 121 TCAGATTTAAATTTGACTCTGGTTGAACAGCCTCAGTTGACGGTGGCTGATGAATTCGC 180
QY 544 CGCGTGTCTCTGACAGGTGGAACAAATTTTCCAAGCAGAGTCCAAATTTCTTTGTGCAG 603

```

```

Db 181 CGGCTGTTCTGTACAGTGGGAACAAATTTTCCAAGCAGAGTCCAAATTTCTTTGTGCAG 240
QY 604 TTTGAAAAGGGATCTGAATATTTTTCATCTGCAACACGCTTGTGAGACCTCCCGCATCTCT 663
Db 241 TTTGAAAAGGGATCTGAATATTTTTCATCTGCAACACGCTTGTGAGACCTCCCGCATCTCT 300
QY 664 TCCATGGTCTCTGGCGGCTACGTGAGTTCAGATTTCGGCCCAAGCTGGTGAAGTGGTCTTC 723
Db 301 TCCATGGTCTCTGGCGGCTACGTGAGTTCAGATTTCGGCCCAAGCTGGTGAAGTGGTCTTC 360
QY 724 CAGGGAATTTGAACCCAGATCAACGACTGGGTGCGCATCACCAAGTAAAGAGGGCGGA 783
Db 361 CAGGGAATTTGAACCCAGATCAACGACTGGGTGCGCATCACCAAGTAAAGAGGGCGGA 420
QY 784 GCGAATAAGGTGGTGGATTCTGGGTATATTTCCCGCTACCTGCTGCCAAGGTCCAAACG 843
Db 421 GCGAATAAGGTGGTGGATTCTGGGTATATTTCCCGCTACCTGCTGCCAAGGTCCAAACG 480
QY 844 GAGCTTCAGTGGGCTGGACAAACCTGGACGAGTATAAATTTGGCCGCCCTGAATCTGGAG 903
Db 481 GAGCTTCAGTGGGCTGGACAAACCTGGACGAGTATAAATTTGGCCGCCCTGAATCTGGAG 540
QY 904 GAGCGCAAAACGCTCGTTCGCGCAGTTTCTGGCAGATCTCTCGCAGGCTCCGAGAGGCG 963
Db 541 GAGCGCAAAACGCTCGTTCGCGCAGTTTCTGGCAGATCTCTCGCAGGCTCCGAGAGGCG 600
QY 964 GCTTCGCGAGCTGAGTTCTCGGCTGACCCGGTCAATCAAAAGCAAGACTTCCAGAAATAC 1023
Db 601 GCTTCGCGAGCTGAGTTCTCGGCTGACCCGGTCAATCAAAAGCAAGACTTCCAGAAATAC 660
QY 1024 ATGGGCTCGTCAACTGGCTGTGGAGCACCGGATCACTTCGAGAAAGCAGTGGATCCAG 1083
Db 661 ATGGGCTCGTCAACTGGCTGTGGAGCACCGGATCACTTCGAGAAAGCAGTGGATCCAG 720
QY 1084 GAAATCAGGAGAGTACTCTCTTCAACTCCACCGGCACTCTCGAGAGCAGATCAAG 1143
Db 721 GAAATCAGGAGAGTACTCTCTTCAACTCCACCGGCACTCTCGAGAGCAGATCAAG 780
QY 1144 GCCGCTCGCAACACGCGATATGATGCTGACAAAAGCGGCTGAGTACTCTC 1203
Db 781 GCCGCTCGCAACACGCGATATGATGCTGACAAAAGCGGCTGAGTACTCTC 840
QY 1204 GTGGGAGCTCCGTTCCGAGGACATTTCAAAAACAGATCTGGGAAATTTTTCAGATG 1263
Db 841 GTGGGAGCTCCGTTCCGAGGACATTTCAAAAACAGATCTGGGAAATTTTTCAGATG 900
QY 1264 AATGGCTACGACCCCGCTACGCGGATCCATCTCTACGGCTGGTCTCAGCGTCTCTTC 1323
Db 901 AATGGCTACGACCCCGCTACGCGGATCCATCTCTACGGCTGGTCTCAGCGTCTCTTC 960
QY 1324 AACAGAGGAACACCGCTCTAGCGACCCGCAACGCGCAAGCAAGCAACATCGCG 1383
Db 961 AACAGAGGAACACCGCTCTAGCGACCCGCAACGCGCAAGCAACATCGCG 1020
QY 1384 GAGGCTATCCGACACTGTGCCCTTTTACGGCTGGTGAATCTGGACCAATGAAATCTTT 1443
Db 1021 GAGGCTATCCGACACTGTGCCCTTTTACGGCTGGTGAATCTGGACCAATGAAATCTTT 1080
QY 1444 CCCTTTAATGACTGTGTGGACAAATGCTCATTTGTTGGGAGGAGGAAGATGACCAAC 1503
Db 1081 CCCTTTAATGACTGTGTGGACAAATGCTCATTTGTTGGGAGGAGGAAGATGACCAAC 1140
QY 1504 AAGTGGTGAATTCGCCAAGGCCATCTCTGGGGGCTCAAAGGTGGGGTCCGATCAGAAA 1563
Db 1141 AAGTGGTGAATTCGCCAAGGCCATCTCTGGGGGCTCAAAGGTGGGGTCCGATCAGAAA 1200
QY 1564 TGTAAATCTCTGTTCAAATGATTTCTACCCCTGTCAATTTGTAATTTCAATCAAAACATG 1623
Db 1201 TGTAAATCTCTGTTCAAATGATTTCTACCCCTGTCAATTTGTAATTTCAATCAAAACATG 1260
QY 1624 TGTGTGGTGGTGGGAAATTCACGACTTTTGAACACAGCAGCGCTGGAGGACCGG 1683

```

Db 1261 TGTGTGGTGGATGGAAATCCAGGACCTTTGAACACGACGCGCTGGAGGACCGC 1320  
QY 1684 ATGTTCAAATTTGAACCTGCTAAGCGGCTCCGCGAGATTTTGGCAAGATTACTAAGCAG 1743  
Db 1321 ATGTTCAAATTTGAACCTGCTAAGCGGCTCCGCGAGATTTTGGCAAGATTACTAAGCAG 1380  
QY 1744 GAACTCAGGACTTTTGTCTTGGGCAAGGTCATCAGGTGCCGGTGACTCAGGATTT 1803  
Db 1381 GAACTCAGGACTTTTGTCTTGGGCAAGGTCATCAGGTGCCGGTGACTCAGGATTT 1440  
QY 1804 AAGTTCCAGGAAATGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCACTG 1863  
Db 1441 AAGTTCCAGGAAATGGCGGAACTAAAGGGCGGAGAAATCTCTAAACGCCACTG 1500  
QY 1864 GGTGACGTACCAATACTAGCTATAAAGTCTGGAGAGGGGCCAGGCTCTCATTTGTT 1923  
Db 1501 GGTGACGTACCAATACTAGCTATAAAGTCTGGAGAGGGGCCAGGCTCTCATTTGTT 1560  
QY 1924 CCGGAGACGCTCGGAGTTTCAGACGTGACTGTTGATCCGCTCCTCTGGACCGCTCAAT 1983  
Db 1561 CCGGAGACGCTCGGAGTTTCAGACGTGACTGTTGATCCGCTCCTCTGGACCGCTCAAT 1620  
QY 1984 TCGAATTCAGGTATGATTCGCAATGTGACTATCATGCTCAATTTGACAAACATTTCTAAC 2043  
Db 1621 TCGAATTCAGGTATGATTCGCAATGTGACTATCATGCTCAATTTGACAAACATTTCTAAC 1680  
QY 2044 AATGTGATGAATGTGAATTTTGAATCGGGGCAAAATGGATGTATCTGTCAATGTA 2103  
Db 1681 AATGTGATGAATGTGAATTTTGAATCGGGGCAAAATGGATGTATCTGTCAATGTA 1740  
QY 2104 ACTCAGTCAATTTGTCTCATGGATTTCCCGCTGGGAAAGGAAAACTTGTGAGATTTT 2163  
Db 1741 ACTCAGTCAATTTGTCTCATGGATTTCCCGCTGGGAAAGGAAAACTTGTGAGATTTT 1800  
QY 2164 GGGATTTTGACGATGCCAATAAAGACAGTAA 2196  
Db 1801 GGGATTTTGACGATGCCAATAAAGACAGTAA 1833

Search completed: December 2, 2004, 21:45:23  
Job time : 12638 secs